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3740, Ap 49, Appli 6, Appli 6,
                                                                                                                                              NAME: Steffe, Eric K.

NAME: Steffe, Eric K.

REGISTRATION NUMBER: 36,688
REGISTRATION NUMBER: 1383.

TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEPAX: 202-371-2543
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 445 amino acids
TYPE: protein

NOLECULE TYPE: protein
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CITY: Washington

CITY: Washington

STATE: DC

COUNTRY: USA

ZIP: 20005-3934

COMPUTER READABLE FORM:

MEDIUM TYPE: Ploppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, 1
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Sequence 5981218

Patent No. 5981218

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Rio, Marie-Christine
APPLICANT: Tomasetto, Catherine
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Matches 135;
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APPLICATION NUMBER: US/08/691,814B FILING DATE: 31-JUL-1996
CLASSIFICATION 435
PRIOR APPLICATION DATA:
APPLICATION UNWBER: US 60/002,183
FILING DATE: 09-AUG-1995
ATTORNEY/ACENT INFORMATION:
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APPLICANT: Byrne, Jennifer
TITLE OF INVENTION: Isolated Nuc
TITLE OF INVENTION: as Leukemia:
NUMBER OF SEQUENCES: 124
CORRESPONDENCE ADDRESS:
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York Ave, N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Release #1.0, Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                  US/08/691,814B
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US-09-949-016-9676

US-09-964-805-2

US-09-949-016-9736

US-09-543-681A-4884

US-09-5252-991A-30190

US-09-252-991A-27075

US-09-949-016-6192
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US-09-241-333-3
US-09-270-767-40232
US-09-270-767-55448
5231168-2
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                                                                                           Score 664; DB 2;
Pred. No. 7.5e-68;
8; Mismatches 45
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NW, Suite 6
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                                                                                                                       Length
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2, Appli
9736, Ap
4884, Ap
30190, A
27075, A
6192, Ap
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3, Appli
40232, A
55448, A
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US-09-949-016-8594
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; ORGANISM: Human US-09-949-016-8594
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GENERAL INFORMATION:
APPLICANT: Lam, Joseph S.
APPLICANT: Burrows, Lori
APPLICANT: Charter, Deborah
APPLICANT: Charter, Deborah
APPLICANT: de Kievit, Teresa
TITLE OF INVENTION: No. 5994072el Proteins Involved in the Synthesis and Assembly
TITLE OF INVENTION: of O-Antigen in Pseudomonas Aeruginosa
FILE REFERENCE: 6580-089
CURRENT APPLICATION NUMBER: US/08/846,762A
CURRENT FILING DATE: 1997-04-30
NUMBER OF SEQ ID NOS: 100
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 92
LENGTH: 341
                                                                                                                                                                                                                                                                                                                                         Sequence 92, Application US/08846762A Patent No. 5994072
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
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Best Local Similarity
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APPLICANT: VENTER,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 8594, Application US/09949016 Patent No. 6812339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: 60/231,498 PRIOR FILING DATE: 2000-09-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS: 207012
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   164 -----AWIETWFLDFKVLPQEAEEENR 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              109 KVLILAYAVCRLRHWWAIALTTAVTSAFLLAKVILSKLFSQGAFGYVLPIISFIL-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             288 VFKGLLWYIVPLVVVYFAEYFINQGLFELLFFWNTSLSHAQQYRWYQM---LYQAGVFAS 344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          110 LIGYAVLQLRHWWVIAVTTLVSSAFLIVKVILSELLSKGAFGYLLPIVSFVLAWLETWFL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       64 LFVTLLWII------ELNVNGGI-----ENTLEKEVMQYDYYSSYFDIFLLAVFRF 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           38;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DFKVLPQEAEEERWYLAAQVAVARGPLLFSGALSEGQFYSPPESFAGSDNESDEEVAGKK
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25.5%;
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Pred. No. 0.41;
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; TYPE: PRT
; ORGANISM: Klebsiella
US-09-489-039A-9711
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                                                                                                                                                                                                                                                                                                            US-09-171-699-4
                                                                                                                                                                                                                                                                                                                            RESULT 5
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CURRENT APPLICATION NUMBER: US/09/489,039A
CURRENT FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 9711
LENGTH: 350
                                                                                                                                                                                                                                      Sequence 4, Application US/09171699
Patent No. 6448389
GENERAL INFORMATION:
APPLICANT: The Wistar Institu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 9711, Application US/09489039A Patent No. 6610836
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Best Local
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local
                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: Howson and Howson
STREET: Spring House Corporate
ZIP: 19477
COMPUTER READABLE FORM:
                                                                                                                                    NUMBER OF SEQUENCES:
                                                                                                                                                                    TITLE OF INVENTION: No. 6448389el
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            111 LILAYAVCRIRHWWAIALTTAVTSAFLLAKVILSKI----FSQGAFGYVLPIISF---IL 163
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                                                                                                                                                                                                                                                                                                                                                                                                                                            83 LILIAVSIPPLAPWWMVVLGTAF--AVVIAKOLYGGLGHNPFNPAMIGYVVLLISFPVOMT 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        47 GISDVRRTFCLFVTFDLLFVTLLWIIELNVNGGIENTLEKEVMQYDYYSSYFDIFLLAVF
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                                              CITY: Spring House
STATE: Pennsylvania
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                                 COUNTRY: USA
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                                                                                                                                                                                                      Berencsi,
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24.0%; Pred. No. 0.62
ative 20; Mismatches
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Pred. No. 1.
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                                                                                                                                                                      Cytomegalovirus DNA Constructs and
                                                                                                                                                                                                                                          Anatomy & Biology
                                                                                   Center,
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.62;
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PCT-US94-02107-2
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                                                                                                                                                                                                                                                                                                       Sequence 2, Application PC/TUS9402107
GENERAL INPRMATION:
APPLICANT: The Wistar Institute of, Anatomy and Biology
TITLE OF INVENTION: Recombinant Cytomegalovirus Vaccine
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
SOPTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/02107
                                                                                                                MEDIUM TYPE: Ploppy
                                                            MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                        STREET: Spring House Corporate Cntr, PO Box 457 CITY: Spring House STATE: Pennsylvania
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Match 6.7%; Score 79.5;
Local Similarity 19.3%; Pred. No. 1.
                                                                                                                                                                                         COUNTRY:
                                                                                                                                                                                                                                                                                     ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: Kodroff, Cathy A.
REGISTRATION NUMBER: 33,980
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/171,699
FILING DATE: 19-Jan-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
DATA:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: WST66APCT TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-540-9200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE DESCRIPTION: SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       321 SPVPATIPLSSVIVAENSDQEESEQSDEEE 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   278 VCSPSVD-----DLRAIAEESDEEEAIVAYTLATR-----GASSSDSLVSPPE 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                157 ---PIISFILAWIETWFLDFKVLPQEAEEENRLLIVQDASERAALIPGGLSDGQFYSPPE 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                227 LSCYVLEETSV-----MLAKRPLITKPEVISVMKRRIEEICMKVFAQ----YILGADPLR 277
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              142 GCSQAMAALQNLPQCSPDBIMAYAQKIFKILDEERDK------VLTHIDHIFMDI 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              69 LWIIELNVNGGIENTLEKEVMQYDY-----YSSYFDIFLLAVFRFKVLILAYAVCRL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14 GSQSSHASLRNIHSINPTQLMARIESY----EGREKKGISDVRRTFCLFVTFDLLFVTL 68
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                                                                                                                                                                19477
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US 60/015,717 FILING DATE: 23-APR-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 215-540-5818
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                                                                                                                                                                                                                                                                                     Howson and Howson
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                                                                                                                                                                                                                 APPLICANT: Furness, Michael
APPLICANT: Buchbinder, Jenny
TITLE OF INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDS
FILE REFERENCE: PA-0041 US
CURRENT PAPLICATION NUMBER: US/09/976,594
CURRENT FILING DATE: 2001-10-12
PRIOR APPLICATION NUMBER: 60/240,409
PRIOR FILING DATE: 2000-10-12
NUMBER OF SEQ ID NOS: 1143
SOFTWARE: PERL Program
SEQ ID NO 503
LENGTH: 723
LENGTH: 723
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Best Local (
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                                              Query Match
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                                                                                                            FEATURE:
NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID No. 6673549 2246292CD1
                                                                                                                                                                              ORGANISM: Homo sapiens
                                                                                                                                                                                                        TYPE: PRT
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APPLICATION NUMBER: US 08
FILING DATE: 12-FEB-1993
ATTORNEY/AGENT INFORMATION:
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LENGTH: 406 amino acid
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y Match 6.7%; Score 79.5; DB 4; Length 723;
Local Similarity 18.0%; Pred. No. 4;
hes 34; Conservative 40; Mismatches 58; Indels 5
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Local Similarity 19.3%; Pred. No. 1.
hes 52; Conservative 36; Mismatche
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TYPE: amino acid
TOPOLOGY: linear
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CLASSIFICATION:
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REFERENCE/DOCKET NUMBER: WS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         142 GCSQAMAALQNLPQCSPDEIMAYAQKIFKILDEERDK------VLTHIDHIFMDI 190
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         57;
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RESULT 9
US-09-270-767-56249
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US-09-270-767-41033
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                                                                                                                                            GENERAL INFORMATION:
APPLICANT: Homburger et al.
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT PILING DATE: 1999-03-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 41033
                                              SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 56249
LENGTH: 221
TYPE: PRT
ORGANISM: Drosophila melanogaster
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                                                                                                                                                                                                                                                                 Sequence 56249, Application US/09270767 Patent No. 6703491
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Best Local (
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 09-270-767-56249
                                                                                                                                         NUMBER OF SEQ ID NOS: 62517
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT ORGANISM: Drosophila melanogaster FEATURE:
                                   FEATURE:
              OTHER INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                            170 FLDFKVLPQEAEEENRLL------IVQDASERAAL--IPGGLSDGQF 208
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          38;
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                Xaa means any amino acid
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Pred. No. 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          73; Indels
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RESULT 11
US-09-724-653-14
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PRIOR FILING DATE: 1999-11-29
NUMBER OF SEQ ID NOS: 20
SOFTWARE: PATENTIN VET: 2.0
SEQ ID NO 2
TENEMEN 7
                                                                                                                                                                                  Sequence 14, Application US/09724653 Patent No. 6830913
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                                                                                                                                                                 GENERAL INFORMATION:
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Best Local S
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                                                CURRENT APPLICATION NUMBER: US/09/724,653
CURRENT FILING DATE: 2000-11-28
PRIOR APPLICATION NUMBER: 60/167,930
                                                                                                      APPLICANT: Ling, Victor
TITLE OF INVENTION: NOVEL ABCB9 TRANSPORTER
FILE REFERENCE; APZ-004CP
SOFTWARE:
               PRIOR FILING DATE: 1
NUMBER OF SEQ ID NOS:
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CURRENT FILING DATE: 2000-11-28
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ORGANISM: Homo
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Pred. No. 5
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RESULT 12
US-09-724-653-15
; Sequence 15, Applica
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US-09-248-796A-20444
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CURRENT FILING DATE: 2000-11-28
PRIOR APPLICATION NUMBER: 60/167,930
PRIOR FILING DATE: 1999-11-29
RUMBER OF SEQ ID NOS: 20
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 15
LENGTH: 766
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LENGTH: 766
TYPE: PRT
ORGANISM: Homo sapiens
                Sequence 20444, Application US/09248796A Patent No. 6747137
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Best Local
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GENERAL INFORMATION:
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Local Similarity 18.0%; Pred. No. 5.7;
hes 34; Conservative 39; Mismatches
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Local Similarity 18.0%; Pred. No. 5.7;
les 34; Conservative 39; Mismatches 59; Indels 5
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FILE REFERENCE: 107196.132
CURRENT APPLICATION NUMBER: US/09/248,796A
CURRENT FILING DATE: 1999-02-12
PRIOR APPLICATION NUMBER: US 60/074,725
PRIOR FILING DATE: 1998-02-13
PRIOR APPLICATION NUMBER: US 60/096,409
PRIOR APPLICATION NUMBER: US 60/096,409
PRIOR FILING DATE: 1998-08-13
NUMBER OF SEQ ID NOS: 28208
SEQ ID NO 20444
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CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILLING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOPTWARE: Patentin Ver. 2.0
SEQ ID NO 43373
LENGTH: 251
TYPE: PRT
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Best Local :
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APPLICANT: Homburger et al.
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                                                                              142 --ALALWIILSCAFGMAANFIPKIYI-----YYISTALFLIFGLKMLYDGYKMKPTDAQB
                                        183 E 183
195 E 195
                                                                                                                           123 WWAIALTTAVTSAFLLAKVILSKLFSQGAFGYVLPIISFILAWIETWFLDFKVLPQEAEE 182
                                                                                                                                                                      104 TASISVILLTELG-
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                                                                                                                                                                                                            63 LLFVTLLWIIELNVNGGIENTLEKEVMQYDYYSSYFDIFLLAVFRFKVLILAYAVCRLRH 122
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                                                                                                                                                                                                                                                                                                                                        6.5%; Score 78; DB 4; Length 251; ilarity 18.8%; Pred. No. 1.3; Conservative 46; Mismatches 63; Indels
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/833,752
FILING DATE: 9-APR-1997
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Altman, Daniel E
REGISTRATION NUMBER: 34,115
REFERENCE/DOCKET NUMBER:
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 355 amino acids
Typer = mino acids
Typer = mino acids
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Search completed: May 17, 2005, 10:22:40 Job time : 37 secs
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Patent No. 6448375
                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 6.5%; Score 78; DB 4; Length 355; Best Local Similarity 23.2%; Pred. No. 2.2; Matches 39; Conservative 25; Mismatches 60; Indels 44;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbe, Martens, Olson & Bear
STREET: 620 Newport Center Drive 16th Floor
CITY: Newport Beach
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: SAMSON, MICHEL
APPLICANT: PARMENTIER, MARC
APPLICANT: VASSART, GILBERT
APPLICANT: LIBERT, FREDERICK
TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR
TITLE OF INVENTION: AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR
NUMBER OF SEQUENCES: 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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ML64_MOUSE
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Q7QIT3
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Result No.

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Minimum Maximum

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Scoring table:

Gapop 10.0 , BLOSUM62

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Post-processing: Minimum Maximum

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RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
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RA Hopkins R.F., Jordan H., Moore T., Rabin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Stapleton M., Ugdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
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RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
"deneration and initial analysis of more than 15,000 full-length human
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Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,

Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,

Rayashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,

Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,

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Ravasi T., Reed J.C., Reed D.J., Stid J., Ring B.Z., Ringwald M.,

Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,

Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,

Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,

Wilming L.G., Wynshaw-Boris A., Yangisawa M., Yang I., Yang L.,

Wan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,

Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,

Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,

Ah Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,

Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,

Ya Birney E., Hayashizaki Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).

SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).

STRAIN=C57BL/6J; TISSUE=Cerebellum, and Kidney;

MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;

MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;

MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;

MEDLINE=22354683; PubMed=12.466851; DOI=10.1038/nature01266;

MEDLINE=22354683; PubMed=10.1038/nature01266;

MEDLINE=22354683; PubMed=10.1038/nature01266;

MEDLINE=22354683; PubMed=10.1038/nature01266;

MAISTOR MAISTOR AND AGAIN AND A
                                                                                                                                                       and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Birney E., Hayashizaki Y.; "Analysis of the mouse transcriptome based on
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
05-JTL-2004 (Rel. 44, Last annotation update)
MLN64 N-terminal domain homolog (STARD3 N-terminal like protein).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
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                                                                SUBCELLULAR LOCATION: Integral men
membrane protein (By similarity).
ALTERNATIVE PRODUCTS:
Event=Alternative splicing; Named
                                              Name=1;
                         IsoId=Q9DCI3-1; Sequence=Displayed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           full-length cDNAs.";
420:563-573(2002).
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Rodentia;
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Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                       membrane
                                                                                                                                   protein.
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RESULT
Q6D138
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Best Local S
Matches 223
Brachydanio rerio (Zebrafish) (
Eukaryota; Metazoa; Chordata; C
Actinopterygii; Neopterygii; Te
Cyprinidae; Danio.
NCBI_TaxID=7955;
[1]
                                                                                                                                                              Q6DI38
Q6DI38;
25-OCT-2004
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25-OCT-2004
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CONFLICT
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                         181
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Note=No experimental confirmation available;
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Cytoplasmic (Potential).

SEEBABEKQESEKPLLEL -> RNSSAFRMGI

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Craniata; Vertebrata; Euteleostomi;
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WARDLINE-22380557; PubMed=12477932; Doi=10.1073/pnas.24260389;

WARDLINE-2280557; PubMed=12477932; Doi=10.1073/pnas.24260389;

WARDLINE-2280557; PubMed=12477932; Doi=10.1073/pnas.24260389;

WARDLINE-2280557; PubMed=12477932; Doi=10.1073/pnas.24260389;

WARDLINE-228057; PubMed=12477932; Doi=10.1073/pnas.
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25-OCT-2004 (TrembLrel. 28, L:
25-OCT-2004 (TrembLrel. 28, L:
25-OCT-2004 (TrembLrel. 28, L:
Stard3-prov protein.
Name=stard3-prov;
Xenopus tropicalis (Western c:
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EMBL; BC07
SEQUENCE
TISSUE-Embryo;
PubMed=12477932; DOI=10.1073/pnas.242603899;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler
Klausner R.D., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.
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Jones S.J., Marra M.A.;
"Generation and initial analysis of more than 15,000 full-length and mouse cDNA sequences.";
and mouse cDNA sequences.";
and watl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                          NCBI :
                                                                                                                                                                                                                                                  SEQUENCE
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Amphibia; Batrachia; Anura;
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BC075752; AAH75752.1; -.
NCE 227 AA; 25485 MW; 24C46AD8FF4985C6 CRC64;
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, Last sequence up
, Last annotation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        clawed frog)
                                                                                                                                                                                                                                                                                                                                                                                                                          Mesobatrachia; Pipoidea;
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Pred. No. 5.1e-64;
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                           N.K.,
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    SEQUENCE FROM N.A.
TISSUE-Spleen;
TISSUE-Spleen;
MEDLINE=23388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
Strausberg R.L., Feingold B.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27,
                                                                                                                                                                                                                                                                                Amphibia; Batrachia; Xenopus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     888
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Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                       MGC68989 protein.
Xenopus laevis (African clawed frog)
                                                                                                                                                                                                                                          NCBI_TaxID=8355;
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InterPro; IPR002913; START.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5
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GO:0017127; F:cholesterol transporter a
GO:0006694; P:steroid biosynthesis; IEA
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c. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
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                                                                                                                                                                                                                                                                                                                         yota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
bia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
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SM00234; START; 1.
B; PS50848; START; 1.
CE 448 AA; 50926 MW;
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Pred. No. 5.2e
29; Mismatches
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Last sequence update)
Last annotation updat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          49;
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J.G.,
M., Schuler G.
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Best Local
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Submitted (SEP-2003) to the EMBL/GenBank/DDE
EMBL; BC057738; AAH57738.1; -.
GO; GO:0015485; F:cholesterol binding; IEA.
GO; GO:0017127; F:cholesterol transporter ac
GO; GO:0006694; P:steroid biosynthesis; IEA.
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to the EMBL/GenBank/DDBJ databases.
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Pred. No. 7.9
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les 51;
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Schein J.E.,
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MGC80895 protein. Name=MGC80895;

MGC80895

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X Strausberg R.L., Peingold E.A., Grouse L.H., Derge J.G.,
X Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
X Klausner R.D., Collins F.S., Wagner L., Shenefer C.F., Bhat N.K.,
X Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
X Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
X Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
X Hopkins R.F., Jordan H., Moore T., Max., Rubin G.M., Hong L.,
X Hopkins R.F., Jordan H., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
X Branes S.S., Loquellano N.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
X Branes S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
X Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
X Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratte P.H.,
X Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gubbs R.A.,
X Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
X Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,
X Pahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
X Milting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
X Milting M., Touchman J.W., Green E.D., Dickson M.C.,
X Hollow D.K., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
X Tones S. J. Marra M. A.
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Matches 139
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
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SMART; SM00234; START; 1.
PROSITE; PS50848; START; 1.
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GO; GO:0015485; F:cholesterol binding; IEA.
GO; GO:0017127; F:cholesterol transporter a
GO; GO:0017127; P:steroid biosynthesis; IEA
InterPro; IPR000799; StART.
InterPro; IPR002913; START.
Pfam; PF01852; START; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Klein 8., Gerhard D.S.;
Submitted (JUN-2004) to the EMBL/GenBank/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-22341132; PubMed=12454917; DOI=10.1002/dvdy.10174; Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
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                                                                                                                                                                                                                                                                                                                          Similarity
PQEAEEENRLLIVQ-DASERAALIPGGLSDGQFYSPPESEAGSE-EAEEKQDS
                                                              IVRLRHWWAIAITTLVTSAFLIVKVIQSGLLSKGAFGYVLPIVSFVLAWLETWFLDFKVL
                                                                                     VCRLRHWWAIALTTAVTSAPLLAKVILSKLFSQGAFGYVLPIISFILAWIETWFLDFKVL
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                                                                                                                                          LFVTFDLLFISLLWIIELNTNNGIEKNLEEBILHYDFKNSFFDIYLLAVFRFSVLILAYA
                                                                                                                                                                                                                                                               MNHLP----EDMENALTGSQSSHASLRNIHSINPTQLMARIESYEGREKKGISDVRRTFC
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                                                                                                                                                                                                                                                                                                                                                                                    448 AA;
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RESOLUTION OF THE STANDARD SERVICE SER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE-Lung, Skin, and Spleen;

RX MEDLINB-22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RX MEDLINB-22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RA Strausberg R.D., Feingold E.A., Grouse L.H., Derge J.G.,

RA Altschul S.F., Zeeberg B., Buerow K.H., Schaefer C.F., Bhat N.K.,

RA Altschul S.F., Zeeberg B., Buerow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsleh F.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M.J., Usdin T.B., Toehiyuki S., Carninci P., Prange C.,

RA Stapleton M.J., Usdin T.B., Toehiyuki S., Carninci P., Prange C.,

RA Stapleton M.J., Usdin T.B., Toehiyuki S., Carninci P., Mullahy S.J.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Raha S.S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Richards S., Worley N.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Richards S., Worley N.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Bouffard G.G.,

RA Rahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

RA Rahey J., Schein A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

"Generation and initial analysis of more than 15,000 full-length human

"Generation and initial analysis of more than 15,000 full-length human

"Generation and sequences.";

"Generation and sequences.";
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30-MAY-2000 (Rel. 39, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
MLN 64 protein (StAR-related lipid transfer protein domain-containing protein 3) (CAB1 protein).
Mame=STARD3; Synonyms=CAB1, MLN64;
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eukaryota; Metazoa; Crordata; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=97413641; PubMed=9270027;
Akiyama N., Sasaki H., Ishizuka T., Kishi T., Sakamoto
Hirai H., Yazaki Y., Sugimura T., Terada M.;
"Isolation of a candidate gene, CABI, for cholesterol
mitochondria from the c-ERBB-2 amplicon by a modified
MEDLINE=21264925; PubMed=11053434; DOI=10.1074/jbc.M006279200; Alpy F., Stoeckel M.-E., Dierich A., Escola J.-M., Wendling C. Chenard M.-P., Vanier M.T., Gruenberg J., Tomasetto C., Rio M. "The steroidogenic acute regulatory protein homolog MLN64, a l
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        method."
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MEDLINE=96039245; PubMed=7490069;
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MEDLINE-20264523; PubMed=10802740; DOI=10.1038/75192;
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                                                                                                                                                                                                                 ., Hurley J.H.;
nd lipid transport mechanism of a StAR-related domain.";
Biol. 7:408-414(2000).
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Pfam; PF01852; START; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL;
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EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          endosomal cholesterol-binding protein.";
J. Biol. Chem. 276:4261-4269 (2001).
-i- FUNCTION: Binds and transports cholesterol. Promotes steroidogenesis in placenta and brain.
-i- SUBCELLULAR LOCATION: Integral membrane protein. Late
                                                                                                                                                                                                                                                                                     PROSITE; PS50848; START; 1.
3D-structure; Lipid transport;
Transmembrane; Transport.
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PIR; I38027; I38027.
PDB; 1EM2; X-ray; A=216-444.
Genew; HGNC:17579; STARD3.
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DATABASE: NAME-Atlas Genet. Cytogenet. Oncol. Haematol.;
WWW-"http://www.infobiogen.fr/services/chromcancer/Genes/MLN64ID202.html".
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GO:0008203; P:cholesterol metabolism;
GO:0006839; P:mitochondrial transport;
GO:0006839; P:steroid metabolism; TAS.
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L; D38255; BAA22525.1; -.
L; BC008365; AAH08356.1; -.
L; BC008747; AAH08747.1; -.
L; BC025679; AAH25679.1; -.
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           MEDIINE-22386257; PubMed=12477932; DOI=10.1073/pnas.242603899; Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Mang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.I. Stapleton M., Soares M.B., Bonaldo M.F., Carninci P., Prange C., Stapleton M.J., Ugdin T.B., Toshiyaki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S. Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hullahy S. Willelman R. M., Markernan K.J., Malek J.A., Gibbe B.
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30-MAY-2000 (Rel. 39, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
MLN 64 protein (Star-related lipid transfer protein domain-containing protein 3) (ES 64 protein).
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MEDLINE=96039245; PubMed=7490069;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
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Rodentia;
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Pred. No. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Craniata; Vert
Sciurognathi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
S., Garcia A.M., G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              62BED5C3EDA0DDEF CRC64;
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thi; Muridae; Murinae; Mus
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  Gay L.J., Hu
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RESULT 9
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Best Local Similarity
Matches 133; Conserv
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                                                                                                                                                                                                                                                                                                                                                         DOMAIN
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakeeley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length huma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRINTS; PR00978; STARPROTEIN. SMART; SM00234; START; 1. PROSITE; PS50848; START; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; X82457; CAA57834.1; -.
EMBL; BC003313; AAH03313.1;
HSSP; Q14849; 1EM2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   entitles requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- FUNCTION: Binds and transports cholesterol. Promotes steroidogenesis in placenta and brain (By similarity).
-!- SUBCELLULAR LOCATION: Integral membrane protein. Late (membrane protein (By similarity).
-!- SIMILARITY: Contains 1 MENTAL domain.
-!- SIMILARITY: Contains 1 START domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro;
                                                                      181
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                                                                                                                                                                                                                                          11 DLERSLPALASIGTSISHSQSLSSHFIPPPL-----EKRRAISDVRRTFCLFVTF
                                                                                             EENRLLIVQDASERAALI-PGGLSDGQFYSPPESEAGSE-EAEEKQDSEK 229
                                                                                                                             HWWVIAVTTLVSSAFLIVKVILSELLSKGAFGYLLPIVSFVLAWLETWFLDFKVLPQEAE
                                                                                                                                             HWWAIALTTAVTSAFLLAKVILSKLFSQGAFGYVLPIISFILAWIETWFLDFKVLPQEAE
                                                                                                                                                                                  DLLFISLLWIIELNTNTGIRKNLEQEVIHYSFQSSFFDIFVLAFFRFSGLLLGYAVLRLQ
                                                                                                                                                                                                    DLLFVTLLWIIELNVNGGIENTLEKEVMQYDYYSSYFDIFLLAVFRFKVLILAYAVCRLR
                                                                                                                                                                                                                                                             DMENAL----TGSQSSHASLRNIHSINPTQLMARIESYEGREKKGISDVRRTFCLFVTF
                                                                        EERWYLAAQAAVARGPLLFSGALSEGQFYSPPESFAGSDNESDEEVTGKK
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IPR002913; START.
                                                                                                                                                                                                                                                                                                    Conservative
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  PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                           MW;
                                                                                                                                                                                                                                                                                                    33;
                                                                                                                                                                                                                                                                                                 Score 656.5;
Pred. No. 5.1e
33; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                    Cytoplasmic MENTAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                            Potential.
Cytoplasmic (Potential).
Potential.
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Potential.
Extracellular (Potential).
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  PRT;
                                                                                                                                                                                                                                                                                                                                                           DBF4359604F3E1E2 CRC64;
  448
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                                                                                                                                                                                                                                                                                                                                                                                                  (Potential)
                                                                                                                                                                                                                                                                                                                 1e-51;
                                                                                                                                                                                                                                                                                                                             DB 1;
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                                                                                                                                                                                                                                                                                                                             Length 446;
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RESULT 10
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Klausner R.D., Collins F.S., Wagner L., Schamer C.M., Schuler G.D.,

A Klausner R.D., Collins F.S., Wagner L., Schamer C.M., Schuler G.D.,

A Altschul S.P., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heiteh F.,

A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heiteh F.,

A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Scheetz T.E.,

Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Stapleton M., J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

A Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

A Blosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

A Blosak S.A., McEwan P.J., McKernan K.J., Malek J.J., Hulyk S.W.,

A Willalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

Villalon D.K., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

A History M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C.,

A Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

Vones S.J., Marra M.A.;

Nones S.J., Marra M.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR000799; StAR.
InterPro; IPR002913; START.
Pfam; PP01852; START; 1.
PRINTS; PR00978; STARPROTEIN.
SMART; SM00234; START; 1.
PROSITE; PS50848; START; 1.
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05-JUL-2004
05-JUL-2004
05-JUL-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Jones S.J., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length and mouse cDNA sequences.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Brachydanio rerio (Zebrafish) (Danio rerio).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GO; GO:0015485; F:cholesterol binding; IEA.
GO; GO:0017127; F:cholesterol transporter a
GO; GO:0006694; P:steroid biosynthesis; IEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; BC056766; AAH56766.1; -. ZFIN; ZDB-GENE-001120-2; stard3.
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Submitted (AUG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=AB; TISSUE=Whole body;
MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
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                                                                                                                                                           163
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                                                                                                                                                                                                                                                                                                                           104 AVFRFKVLILAYAVCRLRHWWAIALTTAVTSAFLLAKVILSKLFSQGAFGYVLFIISFIL
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                                                                                                                                                                                                                                                                                                                                                                                                            43
                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                            AWIETWFLDFKVLPQEAEEEN-RLLIVQDASERAALI-PGGLSDGQFYSPPESEAGSEE 220
                                                                                                                                                                                                                                                                                AVERELCLOLGYAAFRLRHWWVIAITTLVTTAFLIAKVILSDLFSQNAFGYVLPITSEVV
                                                                                                                                                                                                                                                                                                                                                                                                            ERKAPSDVRRTFCLFVTFDLLFITLLWIIELNISKSIWNSLENEVVHYNFKSSFFDIFLL
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(TrEMBLrel.
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Last sequence update)
Last annotation update)
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Pred. No. 1
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Q8BMP8

PRELIMINARY;

PRT;

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EP SEQUENCE FROM N.A.

(C) STRAIN-C579EL/6J; TISSUE=Pituitary gland;

(C) STRAIN-C579EL/6J;

(C) STRAIN-C579EL/GE/C579EL/GE/CT TISTAIN-CT TISTA
SEQUENCE FROM N.A.

C STRAIN-C57BL/61; TISSUE-Pituitary gland;

C STRAIN-C57BL/61; TISSUE-Pituitary gland;

A Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,

A Pukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,

A Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,

A Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,

A Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,

A Katihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,

A Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,

A Nishi K., Nomura K., Numazaki A., Mosato N., Okazaki Y.,

A Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,

A Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.

A Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.

A Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.,

Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
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01-MAR-2003
01-MAR-2003
01-MAR-2003
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STRAIN-C57BL/6J; TISSUS-Pituitary gland;
MEDLINE-20499374; PubMed=11042159; DOI=10.1101/gr.145100;
Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., It
Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
"Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new ge
genome Res. 10:1617-1630(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-MAR-2003 (TREMBLEEL 23, Created)
01-MAR-2003 (TREMBLEEL 23, Last sequence update)
01-MAR-2003 (TREMBLEEL 23, Last annotation update)
01-MAR-2003 (TREMBLEEL 23, Last annotation update)
Mus musculus adult male pituitary gland cDNA, RIKEN full-length
Mus musculus adult male pituitary gland cDNA, RIKEN full-length
enriched library, clone:530402M06 product:H NH1021A08.1 PROTEIN
(UNKNOWN) (PROTEIN FOR MGC:14607) (SIMILAR TŌ STEROIDOGENIC ACUTE
REGULATORY PROTEIN RELATED) homolog.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=Pituitary gland;
MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        the RIKEN Genome Exploration Research Group "Analysis of the mouse transcriptome based 60,770 full-length CDNAs.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. STRAIN=C57BL/6J; TISSUE=Pituitary
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TISSUE=Pituitary gland;

TOTAL DOI:1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RIKEN FANTOM Consortium; "Functional annotation o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=C57BL/6J; TISSUE=Pituitary gland;
MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus (Mouse).
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Sciurognathi; Muridae;
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on functional annotation
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ka T.,
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PROSITE; PS50848; START; 1.
NON_TER 1
NON_TER 568 568
SEQUENCE 568 AA; 62932 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Anopheles Genome Sequencing Consortium;
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
-i- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry v
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Anopheles gambiae str. PEST.
Eukaryota; Metazoa; Arthropoda; Hexapoda; Inse
Neoptera; Endopterygota; Diptera; Nematocera;
NCBI_TaxID=180454;
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01-MAR-2004
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InterPro; IPR002913; START.
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GO:0017127; P:cholesterol transporter activity; IEA
GO:0006694; P:steroid biosynthesis; IEA.
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; AAAB01008807; EAA03945.1;
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                                                                                                                                                ------GGLSD--GQFYSPPES--EAGSEEAEEKQDSE
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Last annotation updat
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Pred. No. 6.7e-23;
5; Mismatches 72
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Pred. No.
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RA Adams N.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., Ra Amanstides P.G., Scherer S.E., Li P.W., Hoskins R.A., Gocayne J.D., Ra George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., Ra George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., Ra George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., Ra George R.A., Calle R.F., Ra George R.G., Champe M., Pfeiffer B.D., Ra George R.G., Rompe M., Pfeiffer B.D., Ra Barton R.C., Rogers Y.H., Blazej R.G., Champe M., Pfeiffer B.D., Ra Barton R.C., Rogers Y.H., Blazej R.G., Champe M., Pfeiffer B.D., Ra Barton R.C., Rogers Y.H., Blazej R.G., Champe M., Pfeiffer B.D., Ra Bartis R.G., Baster E.G., Helt G., Nelson C.R., Gabor G.L., Ra Bartis R.C., Besons P.V., Berman B.P., Bandari D., Bolshakov S., Ra Bartis R.C., Busem D.A., Butler H., Cadieu E., Center A., Chandra I., Ra Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S., Delcher A., Deng Z., Mays A.D., Dew I., Davies P., Ra Gerbios B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M., Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., Ra Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M., Ra Fosler C., Gabrielian R.E., Garg N.S., Gelbart W.M., Glasser K., Ra Harris N.L., Harvey D., Heiman T.J., Herinafez J.R., Houck J., Ra Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibeyam C., Mila S., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z., Lako P., Levitsky A.A., Li J., Li Z., Liang Y., Lin X., Lako P., Levitsky A.A., Li J., Li Z., Liang Y., Lin X., Lako P., Levitsky A.A., Li J., Li Z., Liang Y., Lin X., Lako P., Levitsky A.A., Marphy B., McPherson D., McPherson D., McPherson D., P., Wei M.H., Wassen D.L., Mosler R.A., Nixon K., Musskern D.R., Scheeler F., Shen H., Ra Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H., Ra Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H., Ra Ra Reinert K., Woodager, Worley R.C., Stapleton M., Strong K., Wang A.H., Wang X., Wang S., Yao Q.A., Ye J., Ra Ra Ra Ra Ra Ra Ra 
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01-OCT-2002 (TrEMBLrel
25-OCT-2004 (TrEMBLrel
LD23890p (CG3522-PB).
ORFNames=CG3522;
            Celniker S.E., Wheeler D.A., Kromniller B., Carlson J.W., Halpe, Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A. George R.A., Hoskins R.A., Laverty T., Muzny D.M., Nelson C.R., Pacleb J.M., Park S., Pfeliffer B.D., Richards S., Sodergren E.J. Svirskas R., Tabor P.B., Wan K., Stapleton M., Sutton G.G., Venu Weinstock G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M., "Finishing a whole-genome shotgun: Release 3 of the Drosophila melanogaster euchromatic genome sequence.";
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Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7227
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Celniker S.;
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Eukaryota; Metazoa; Arthropoda;
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                                                                                                                                                                                                                                            Science
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euchromatic genome sequence.";
3:RESEARCH0079-RESEARCH0079(2002)
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ORFNames=CG3522

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EMBL; AB003464; AAS64770.1; -.
FlyBase; FBgn0035028; CG3522.
GO; GO:0015485; F:cholesterol b
GO; GO:0017127; F:cholesterol t
GO; GO:0016694; P:steroid biosy
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InterPro; IPR002913; START.
PRINTS; PR000978; STARPROTEIN.
PROSITE; PS50848; START; 1.
SEQUENCE 545 AA; 61429 MW;
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Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Camp Misra S., Crosby M.A., Mungall C.J., Milburn G.H., Pro Smith C.D., Tupy J.L., Whitfied E.J., Bayraktaroglu L., Smith C.D., Tupy J.L., Whitfied E.J., Bayraktaroglu L., Bettencourt B.R., Celniker S.E., de Grey A.D., Drysdale Harris N.L., Richter J., Russo S., Schroeder A.J., Shu Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rub
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FlyBase;
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Ashburner M., Celniker S.
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SEQUENCE FROM N.
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                                              E--AEEENRLLIVQDAS--ERAALI----
                                                                                               SITALSTSGSCLFLISKVFVFDWLDSK---QQVFEVILIITSFILAWGEAWFLDCRVIPQ
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R.A.,
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Eukaryota;

Metazoa; Arthropoda; Hexapoda; Insecta;

Pterygota;

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RA Abril J.F., Agbayani A. An H.J., Andrews-Pfannkoch C., Baldwin D., RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M., RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S., RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S., RA Borkova D., Bocchan M.R., Bouck J., Brokstein P., Brottier P., Rottier P., Ra Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., Davies P., Dodoson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., RA Dodson K.J., Bvangelista C.C., Ferraz C., Ferriera S., Fleischmann W., RA Durbin K.J., Bvangelista C.C., Ferraz C., Ferriera S., Fleischmann W., RA Durbin K.J., Bvangelista C.C., Ferraz C., Ferriera S., Fleischmann W., RA Hortin D., Houston K.A., Howland T.J., Hernandez J.R., Houck J., Lin X., RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z., Liang Y., Lin X., RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z., Liang Y., Lin X., RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z., Liang Y., Lin X., RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A., RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Nushrefi A., RA Reinert K., Renington K.A., Nixon K., Nusskern D.R., Pacleb J.M., RA Reinert K., Renington K.A., Saunders R.D., Scheeler F., Shen H., RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T., RA Wang Z.Y., Wassarman D.A., Weinstock G.M., Weissenbach J., RA Wang Z.Y., Wassarman D.A., Weinstock G.M., Weissenbach J., RA Wang Z.Y., Wassarman D.A., Weinstock G.M., Weissenbach J., RA Scheng K.H., Zhong F. N., Zhong G., Zhou X., Zhu S., Zhu X., Smith H.O., Ra Globs R.A., Myers E.W., Rohin G.M., Venter J.C.;

"The genome sequence of Drosophila melanogaster.";
                                               MEDLINE=22426069; Misra S., Crosby M
Misra S., Crosby M
Hradecky P., Huang
Smith C.D., Tupy J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-22426065; PubMed-12537568;
Celniker S.E., Wheeler D.A., Krommiller B., Carlson J.W., Halpern Celniker S.E., Modgson A.,
Patel S., Adams M., Champe M., Dugan S.P., Frise B., Hodgson A.,
George R.A., Hoskins R.A., Laverty T., Muzny D.M., Nelson C.R.,
Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Vente:
Weinstock G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.;
"Finishing a whole-genome shotgun: Release 3 of the Drosophila
melanogaster euchromatic genome sequence.";
Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
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"The transposable elements
a genomics perspective.";
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Ephydroidea; Drosophilidae; Drosophila.
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2426069; PubMed=12537572;
Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S., P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.B., Tupy J.L., Whittied E.J., Bayraktaroglu L., Berman B.P. rt B.R., Celniker S.E., de Grey A.D., Drysdale R.A.,
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                                                                                                                                                                                                                                                                                                                                                                                  Drosophila melanogaster
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Reese M.G.,
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                                                                   Caenorhabditis elegans.
Caenorhabditis elegans.
Nematoda;
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01-NOV-1996 (TrEMBLrel.
01-OCT-2002 (TrEMBLrel.
01-MAR-2004 (TrEMBLrel.
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GO; GO:0015485; F:cholesterol binding; IGO; GO:0017127; F:cholesterol transporte GO; GO:0006694; P:steroid biosynthesis; InterPro; IPR000799; START.
InterPro; IPR002913; START.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PubMed=14745013; DOI=10.1073/pnas.0308212100; Roth G.E., Gierl M.S., Vollborn L., Meise M., Lin "The Drosophila gene Startl: a putative cholester key regulator of ecdysteroid synthesis."; Proc. Natl. Acad. Sci. U.S.A. 101:1601-1606(2004)
SEQUENCE FROM N.A. STRAIN=Bristol N2; MEDLINE=99069613;
                                                         Eukaryota; Metazoa; Nemat
Rhabditidae; Peloderinae;
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                                             NCBI_TaxID=6239;
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AY455866; AAR19767.1; -.
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M.S., Vollborn L., Meise M., Lintermann R., Korge G.;
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Matches 56
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Q90ZB9;
28-FEB-2003
                                                                                                                                                                                                       28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
MIN64-11ke protein (Fragment).
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                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Protacanthopterygii; Salmoniformes; Salmonidae; Salvelinus.
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SMART; SM00234; START; 1.
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STRAIN-Bristol N2;
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STRAIN-Bristol N2;
                                          NCBI_TaxID=8038;
                                                                                                                                                               Salvelinus fontinalis (Brook trout) (Brook char).
                                                                                                                                                                                           Name=MLN64;
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WormPep; F26F4.4; CE30767.
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C;Genetics:	conserved hypothet	F72342	276 2	5.1	61.5	1489	
A;Cross-ret	hypothetical prote	T28980			61.5	1487	
A;Residues:	hypothetical prote	G82888		5.1	61.5	. 1486	
Molecul	hypothetical prote	T18998		5.1	61.5	1485	
A:Status: D	hymothetical prote	T19811			л o	1484	
A;Reference	nucleoplasmin A -	A26630			61.5	1482	
~		H69327		5.1	61.5	1481	
submitted t	hypothetical prote	H70478		л u	7 . 7 .	1480	
C;Accession	hypothetical prote	G89947		n (1	61.5	1478	
C;Date: 20-	hypothetical prote	H97775		5.1	61.5	1477	
C;Species:	epithelial membran	JC5045		5 .	61.5	1476	
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#16170 ##WOLT X	hypothetical prote	877185		n 51	61.5	1473	
	probable NADH2 deh	843955		•	61.5	▲.	
	hypothetical prote	C86655		•	61.5	1471	
ם מם	hypothetical prote	E69985		5	61.5	7	
X	hypothetical prote	B99233			61.5	1469	
	hacitracin symthet	T31679		л u s k	N 0	146/	
١ مم	hypothetical prote	T20695		1 U1	5 2	1466	
!	sodium channel pro	A60165		•	62	1465	
Q 1	hypothetical prote	T18939			62	1464	
ţ	unknown protein F2	C96767			60	1463	
子	nypochecical proce	C88480			n 0	1461	
Ş	hypothetical prote	T43458		•	S 8	1460	
ı	Rab6 GTPase activa	T13163		•	62	1459	
Db	acriflavin resista	AE3557		•	62	1458	
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9	Ca2+-transporting	PWBYR1			62	1456	
Haccino	penicillin-binding	C70191			200	1455	
Best Loca	97K alpha trans-in	TNBEEH			62	1453	
Query Mat	tegument protein 1	T42556		5.2	62	1452	
	aminopeptidase N [E95092			62	1451	
A;Gene: MLN	vacuolar assembly	T09455			62	1450	
A;Note: sur	cytochrome-c oxida	A46616		•	3 8	1448	
A; Cross-ref	protein H06H21.10	A88679		•	62	1447	
A;Residues:	probable ABC trans	873829			626	1446	
A;Scatus: F	nypothetical prote	125050		•	n 0	1444	
A; Accession	heat shock protein	HHMS84		•	5 2	1443	
A;Reference	nucleolin - human	A35804		•	62	1442	
A; Title: Id	hypothetical prote	T03903			62	1441	
Genomics 28	hypothetical prote	F71921			62	1440	
C;Accession	pnospnotransierase	546952		•	n 6	1436	
C;Date: 01-	hypothetical prote	T20799		•	62	1437	
C;Species:	amino acid transpo	A44432			62	1436	
MIN 64 prot	hymothetical prote	T20034		•	5 6	1414	
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	•	AD3138		•	62	1432	
	hypothetical prote	T02360		•	62	1431	
	hypothetical prote	\$19424			62	2	
	procesn &z - Acyrc	529498			5 6	1429	
	nicotinic acetylch	ACCH2N		•	62	4 2	
	tran	A96671		•	62	1426	
		AE2372			62	1425	
	probable menurame	B81914		•	, v	1424	
	NADH2 dehydrogenas	853834	497	•	62	1422	
	e 3-oxoacy	T05271		•	62	1421	
	nuclear protein EN	846124			62	42	
1491 6	hypothetical prote	E64232	456 2	л U	5 6	1418	
1490 6	probable replicati	A84487		•	62	1417	_
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ption: The sequence of C. elegans cosmid F26F4.
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glucose-1-phosphate thymidylyltransferase related protein PAB2433 - C;Specias: Pyrococcus abyssi C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-JC;Accession: D75080 R;anonymous, Genoscope
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Jong, I.; Jeffries, A.C.; Kozera, C.J.;
arrett, R.A.; Ragan, M.A.; Sensen, C.W.;
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C;Species: Sulfolobus solfataricus
C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 09-Jul-2004
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A; Residues: 1-348 < KUR>
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A;Introns: 47/2; 81/2; 125/3; 171/3; 214/1; 236/2; 343/3; 444/1
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   Data Library,
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23.7%;
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Pred. No. 2.7e-11;
   July 1999
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calcium channel alpha-1 chain - Cyanea capillata (;Species: Cyanea capillata C;Species: Cyanea capillata C;Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 09-Jul-2004 C;Accession: T43048 R;Jeziorski, M.C.; Greenberg, R.M.; Clark, K.S.; Anderson, P.A.V. J. Biol. Chem. 273, 22792-22799, 1998 A;Title: Cloning and functional expression of a voltage-gated calcium channe A;Title: Cloning and functional expression of a voltage-gated calcium channe A;Reference number: Z22300; MUID:98380510; PMID:9712913 A;Accession: T43048
                                                                                                                                                                                                                                                                                                                                                                                   A;Residues: 1-1911 <JEZ>
A;Residues: 1-1911 <JEZ>
A;Cross-references: UNIPROT:002038; EMBL:U93075; NID:g1947095; PID:g1947096; PIDN:AAC6305
C;Superfantly: voltage-dependent calcium channel protein alpha-1 chain
C;Keywords: transmembrane protein
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A;Reference number: A75001
A;Accession: D75080
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C; Superfamily:
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A;Molecule type: DNA
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Pred. No. 0.59
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RESULT

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probable molybdopterin biosynthesis protein Cj1519 [imported] - Campylobacter jejuni C;Species: Campylobacter jejuni C;Pate: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 16-Aug-2004 C;Accession: B81299
R;Parkhill, J:; Wren, B.W.; Mungall, K.; Ketley, J.M.; Churcher, C.; Basham, D.; Chillin C.W.; Quail, M.; Rajandream, M.A.; Rutherford, K.M.; VanVliet, A.; Whitehead, S.; Barrel Nature 403, 665-668, 2000
A;Title: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals hyp A;Accession: B81299
A;Accession: B81299
A;Status: preliminary A;Genetics: DNA
A;Residues: 1-396 < PAR> A;Gross-references: UNIPROT:09PME5; GB:AL139078; GB:AL111168; NID:g6968723; PIDN:CAB7393
A;Experimental source: serotype O2, strain NCTC 11168
C;Genetics: moeA2; Cj1519
C;Superfamily: Molybdenum cofactor molybdenum incorporation protein MoeA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Reference number: Z19495
A;Accession: T21969
A;Status: preliminary; translated from A;Molecule type: DNA
A;Residues: 1-767 <WIL>
A;Cross-references: UNIPROT:Q20170; EN
A;Experimental source: clone F38E11
C;Genetics:
A;Gene: CESP:F38E11.7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hypothetical protein F38E11.7 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004 C;Accession: T21969
R;Matthews, P.
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A; Introns: 50/2; 118/1; 139/2; 189/3; 226/1; 248/1; 287/2; 375/2; 432/3; 465/3;
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                                                                                                                                                                                                                                                                                                                Query Match
Best Local
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Best Local
                                                                                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                           185
                                             101 PLLAV--FRFKVLILAYAVCR--LRHWWAIALTTAVTSAFLLAKVILSKLFSQGAFGYVL 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 FDLLFVTLLWIIELNVNGGIENTLEKEVMQYDYYSSYFDIFLLAVFRFKVLIL---AYAV 117
                                                                                                                                                                                                                                         4 LPEDMENALTGSQSSHASLRNIHSINPTQLMARIESYEGREKKGISDVRRTFCLF----
                                                                                                                                                                                                                                                                                           47;
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                                                                                                                                           VTFDLLFVTLLWIIELNVNGGIE----NTLEKEVMQYDYYSSYFDI------
                                                                                                                                                                                           LGEALENPAQIRSSNHIAIANL-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CRLRHWW---
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  FIIALPGFPYSAMVMFNLYTREILNSW----
                                                                                             ATFSTLESALQSCDILVTTGGVSMGDFDFLKKAIKEYEIIIDKADIKPGRHIKIAKANEK
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                                                                                                                                                                                                                                                                                                             7.2%; Score 85.5; DB 2;
21.0%; Pred. No. 3.1;
                                                                                                                                                                                                                                                                                           35; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 86.5;
Pred. No. 5.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ---AIALTTAVTSAFLLAKVILSKLFSQGAFGYVLPI 158
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                                                                                                                                                                                                                                                                                         81;
                                                                                                                                                                                              ----AKNLNCDTRVFPLLKDDEK
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  -LLQPKDYICKAFLQGSYKKKT 333
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C; Species: Bo:
C; Date: 13-Fel
C; Accession: (
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C;Date: 10-Nov-1995 ;
C;Accession: A57219
R;Lerner, T.J.; Boust
                                                                                                                                                                                                                                                                                                      Nature 390, 580-586, 1997
A;Authors: Smith, H.O.; Venter, J.C.
A;Title: Genomic sequence of a Lyme disease spirochaete,
A;Reference number: A70100; MUID:98065943; PMID:9403685
                                                                                                                                                                                                                                                                                                                                                                                              R;Fraser, C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, R.; son, D.; Peterson, J.; Kerlavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.; Bowman, C.; Garland, S.; Fujii, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hatch,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: GDB:120593; OMIM:204200
A;Map position: 16p12.1-16p11.2
C;Superfamily: Clu3 protein/Battenin/Batten disease protein/BTN1 protein
C;Keywords: membrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cell 82, 949-957, 1995
A;Title: Isolation of a novel gene underlying Batten disease,
A;Reference number: A57219; MUID:96016090; PMID:7553855
片
                              S
                                                                                                                                                                               A;Cross-references: UNIPROT:O51531; GB:AE001160; GB:AE000783; A;Experimental source: strain B31
                                                                                                                                                                                                                         A; Molecule type: DNA
A; Residues: 1-448 < KLE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       conserved hypothetical integral membrane protein BB0584 - Lyme disease spirochete
C;Species: Borrelia burgdorferi (Lyme disease spirochete)
C;Date: 13-Feb-1998 #sequence_revision 13-Feb-1998 #text_change 09-Jul-2004
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A; Residues: 1-438 < LER>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Batten disease-related protein CLN3 - C; Species: Homo sapiens (man)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      밁
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Cross-references:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;Species: Homo sapiens (man)
;Date: 10-Nov-1995 #sequence_revision 10-Nov-1995 #text_change 16-Aug-2004
                                                                                                                                  Query Match
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271 DTHKYAAYSISFSIYFIIFNIIHSFCISLNIMMGYEMHNSKKEIMKVAIYLSKIGLKLAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        109 KVLILAYAVCRLRHWWAIALTTAVTSAFLLAKVILSKLFSQGAFGYVLPIISFIL----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     277 VFKGLLWYIVPLVVVYFAEYFINQGLFELLFFWNTSLSHAQQYRWYQM---LYQAGVFAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               64 LFVTLLWII------ELNVNGGI-----ENTLEKEVMQYDYYSSYFDIFLLAVFRF 108
                                                                                      l Similarity
47; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
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                                          DVRRTFCLEVTEDLLEVIL----LWIIELNVNGGIE-WILEKEVMQYDYYSS-----Y
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                                                                                    7.1%;
larity 24.4%;
Conservative 2
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25.5%;
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                                                                                        28;
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                                                                                                           Score 85;
Pred. No.
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Pred. No. 3.
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                                                                                                                                  2
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                                                                                           64;
                                                                                                                                  Length 448
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    330
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probable integral membrane protein [imported] - Clostridium acetobutylicum C;Species: Clostridium acetobutylicum C;Species: Clostridium acetobutylicum C;Species: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 09-Jul-2004 C;Accession: H97002 R;Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; L.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R. J. Bacteriol. 183, 4823-4838, 2001 A;Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium A;Reference number: A96900; MUID:21359325; PMID:21359325 A;Accession: H97002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 11
H97002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R; Kuge, O.; Nishijima, M.; Akamatsu, Y.
J. Biol. Chem. 266, 24184-24189, 1991
A; Title: A Chinese hamster cDNA encoding a A; Reference number: A41680; MUID:92084729; A; Accession: A41680
                                                                                                                                                                          A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-352 <KUR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: GB:D10234; GB:D90468; NID:g220280; PIDN:BAA01084.1; PID:d1001553; C;Superfamily: Caenorhabditis elegans hypothetical protein ZC506.3 C;Keywords: membrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-471 <KUG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                integral membrane protein pssA - Chinese hamster C;Species: Cricetulus griseus (Chinese hamster) C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992
                                                                                                            A; Experimental source: C; Genetics:
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                                                                                                                                 Cross-references: UNIPROT:Q97KT1; GB:AE001437; PIDN:AAK78811.1; PID:g15023727; GSPDB:
Experimental source: Clostridium acetobutylicum ATCC824
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Best Local :
    Matches
                       Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   98
    38;
                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7.1%;
Similarity 24.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AECWWDQVILD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILFLNFEQVKSLMYW-LDPNLRYA---TREADIMEYAVNCHVITWERIVSHFDIFAFGH 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FCLFVTFDLLFVTLLWIIELNVNGGIENTLEKEVMQY-----DYYSSYFDIFLLAV 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FWGWAMKALLIRSYGLC----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          F----RFKVLILAYAVCRLRHWWAIALTTAVTSAFLLAKVILSKLFSQGAFGYVLPIISF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FDIFLLAVFRFKVLILAYAVCRLRHWWAIALTTAVTSAFLLAKVI--LSKLFSQGA----
    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -FGYVLPIISFILAWIETWFLDFKVLPQEAEEENRLLIV-----QDASERAA 197
7.0%; Score 83.5; 1
19.2%; Pred. No. 4.1
tive 35; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      210
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 84.5; DB 2;
Pred. No. 4.7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        protein essential PMID:1748687
                                           DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  #text_change 06-Oct-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 471;
                                           Length
    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     --IIVFIPSLEDAIKLVV 434
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             39;
  75;
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  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Species: Yersinia pestis
C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004
C;Accession: AE0302
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AE0302
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                                                                                                                                                                                                                                                                                                                                                                           A;Gene: YPO2476
C;Superfamily: inner membrane protein ugpA
                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: DNA
A; Residues: 1-291 < KUR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Title: Genome sequence of Yersinia pestis, the causative A;Reference number: AB0001; MUID:21470413; PMID:11586360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     밁
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Accession: AE0302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sugar ABC transporter, permease protein YPO2476 [imported] - Yersinia pestis
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                                                                                                                                                                                                                                                                                                                       Local
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                                                                                                                                                69 MINVMRPIMY--YLPIVEISSFLF----AFGLQKLKHG-----RTFVALSFILLANVSSG 116
                                                                                                                                                                                   85 EKEVMOYDYYSSYFDIFLLAVFRFKVLILAYAVCRLRHWWAIALTTAVTSAFLLAKV---
                                                                                                                                                                                                                                                                46
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                                                                                                                                                                                                                                                                                                   44;
                                                                                                                                                                                                                                                                                                                       Similarity
                                                                        VAYSIVESKIESQNGPLNTELYDWEGETLEWLTSPDEAMLSIALVVTWKEVGYYGLILES 176
                                                                                                                                                                                                                                                              KGISDVRRTFCLFVTFDLLFVTLLWIIELNVN---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VVNGAVIIRDREENTYYRYMYSPNSKFEYIFGNVIYNYIFSYIQLFIANSLMAIFGIYIG
 GLNSIPKEIYSAAELDN
                                   DFKVLPQE----ABEEN 184
                                                                                                             ----FILSKLFSQGA-----FGYVLPIIS-----FILAWIETW-----FL
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                                                                                                                                                                                                                           KOVGSVLAASYLGYTSIFWFYPFIWLAVLSLTEWRFVGIPTFNGLNNFILVMODPLFWKS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          I-----LAYAVCRIRHWWAIALTTAVTSAF-----LLAKVILSKLFSQGAFGYVLPIIS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ESYEGREKKGISDVRRTFCLFVTFD-----
                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                6.9%; orc. No. ...
22.3%; pred. No. ...
--ive 26; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ---ILTLVMTTFGTFIVCIFNKELYANMFSAA-----IS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                294
                                                                                                                                                                                                                                                                                                                       DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                PIDN:CAC91281.1; PID:g15980470; GSPDB:G
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                                                                                                                                                                                                                                                                                                     57;
                                                                                                                                                                                                                                                                  -----GGIENTL---
                                                                                                                                                                                                                                                                                                                                        Length
                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                          291;
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                                                                                                                                                                                                                                                                                                     70;
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                                                                                                                                                                                         141
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                                                                                                                                                                                                                                                                                                         10,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (strain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ntice, M.B.;
bugan, G.; I
Barrell, I
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NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 5 - Crithidia oncopelti C;Species: mitochondrion Crithidia oncopelti C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004 C;Accession: S34960 R,Maslov, D.A.; Horvath, A.; Gwang II, K.; Kolesnikov. A.A.

mitochondrio

.; Gwang II, K.; Kolesnikov, Library, October 1990

RESULT 13

A; Molecule type: DNA
A; Residues: 1-590 < MAS>
A; Cross-references: UNI
C; Genetics:

UNIPROT: Q34192; EMBL: X56015; NID: g12879; PIDN: CAA39492.1; PID: g12882

R;Maslov, D.A.; Horvath, A.; submitted to the EMBL Data L: A;Reference number: S34958

A; Accession: S34960

S .. - 134

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A;Gene: ND5
A;Genome: mitochondrion
A;Genome: code: SGCG
A;Genetic code: SGCG
C;Superfamily: NADH dehydrogenase (ubiquinone) chain 5
C;Keywords: membrane-associated complex; mitochondrion; NAD; oxidative phosphorylation;
C.A.; Venter, J.C.
Science 270, 397-403, 1995
A;Title: The minimal gene complement of Mycoplasma genitalium.
A;Reference number: A64200; MUID:96026346; PMID:7569993
A;Accession: C64227
A;Status: preliminary; nucleic acid sequence not shown; translation
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R;Finlay, B.B.; Paranchych, W.
J. Bacteriol. 166, 713-721, 1986
A;Title: Nucleotide sequence of the surface exclusion genes traS and traT from the IncF-A;Reference number: A29835; MUID:86223783; PMID:3011738
A;Accession: B29835
A;Btatus: preliminary
A;Molecule type: DNA
A;Residues: 1-186 <FIN>
A;Residues: 1-186 <FIN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tras protein - Escherichia coli plasmid pED208
C;Species: Escherichia coli
C;Date: 04-Aug-1988 #sequence_revision 04-Aug-1988 #text_change 09-Jul-2004
C;Accession: B29835
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B29835
                                                                                                                                                               R;Fraser, C.M.; Gocayne, J.D.; White, O.; Adams, M.D.; Clayton, R.A.; Fleischmann, M.; Fuhrmann, J.; Nguyen, D.; Utterback, T.R.; Saudek, D.M.; Phillips, C.A.; Merri, C.A.; Venter, J.C.
                                                                                                                                                                                                                                            hypothetical protein homolog MG247 - Mycoplasma genitalium C;Speckes: Mycoplasma genitalium C;Speckes: Mycoplasma genitalium C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004 C;Accession: C64227
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C;Genetics:
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Best Local S
Matches 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 6.9%; Score 82.5; DB 2; Length 186; Best Local Similarity 23.8%; Pred. No. 2.4; Matches 31; Conservative 24; Mismatches 40; Indels 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         188 STGYGMINFYFVNF 201
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       166 IETWFLDFKV 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            167 ET-----WFLDF 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  147 SF--FLISY-----FWYRFFALKFGFKSFFISKI------GDVLLLLSFVMTFI 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  107 RFKVLILAYAVCRLRHWWAIALTTAVTSAFLLAKVILSKLFSQGAFGYVLPIISFILAWI 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             116 AVCRIRHWWAIALTTAVTSAFLLAKVILSKLFSQGAFGYVLPII------SFILAW 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             88 NLVSLK----ISLGSEITEQSVLLKLVERKINSYGQFLMVVNAIVGCVLLSSGERFVAGL 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 FDLLFVTLLWIIELNVNGGIENTLEKEVMQYDYYSSYFDIFLL-----AVFRFKVLILAY 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           95 FILFYAFYYMYYDLMLKRFFNIFWWFVLCMNFFI-----LSYDYLTAYCGWELLGLF 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 55 FCLFVTF-----DLL---FVTLLWIIELNVNGGIENTLEKEVMQYDYYSSYFDIFLLAVF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FQLLFI----IFDIFINSNVR-----DYH--YFDTFVITLGSNAFFSLVFLMSTY
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                                  not shown
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A;Residues: 1-239 <TIGR>
A;Cross-references: UNIPROT:P47489; GB:U39703; GB:L43967; NID:g3844835; PIDN:AAC71467.1;
A;Experimental source: strain G-37
C;Genetics:
A;Genetic code: SGC3
C;Superfamily: Escherichia coli ygiH protein
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                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                         Query Match
Best Local 9
159 VSLASLITF---
                                136 FLLAKVILSKLFSQGAFGYVLPIISFILAWIE 167
                                                                                                     93 YYSSYFDIFLLAV-----FRFK----VLILAYAVCRLRHWWAI-----ALTTAVTSA 135
                                                                                                                                      42 GSKNPGATNSMRVFGLKIGFLVAIFDAFKGFFAFLLTWIL---FRFGLQGYLTEKVYQST
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Search completed: May 17, 2005, 10:23:07 Job time : 35 secs

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                                                                             ABB84847 standard; protein; 234 AA. Human PRO1864 protein sequence SEQ WO200200690-A2.
ABB95453 standard; protein;
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SUMMARIES
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13-FEB-2003
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Human PRO polypeptide #33.
US2003036140-A1.
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                                                    ABR98774 standard; protein; Human secreted polypeptide US2003040064-A1.
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Human secreted polypeptide I
US2003040063-A1.
27-FEB-2003.
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Human secreted/transmembrane
US2003009013-A1.
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Novel human secreted and transmembrane
US2003018183-A1.
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Human secreted polypeptide PRO1864,
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         ABU88685 standard;
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                  ABU71512 standard; protein;
Human secreted polypeptide I
                                                                                        ABO13698 standard; protein; 234 AA.
Human secreted/transmembrane protei
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Human PRO1864 protein. US2003036143-A1. 20-FEB-2003.
                                                                                                                 Human PRO polypeptide #33.
US2003032102-A1.
13-FRB-2007
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US2003032117-A1.
                                                         Novel human secreted and tra
US2003036117-A1.
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Human secreted/transmembrane
US2003022298-A1.
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US2003045684-A1.
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ID ABU79201 standard; p
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US2003032110-A1.
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US2003022293-A1.
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US2003036150-A1.
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ABU91386 standard; protein;
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US2003068682-A1.
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Human secreted polypeptide
US2003068752-A1.
                                                                                                                                                                                                          ABO31502 standard; protein; 234 AA. Human secreted/transmembrane protei US2003068725-A1.
                                                                                                                                                                                                                                                                                     Human secreted/transmembrane US2003068685-A1.
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Human secreted polypeptide |
US2003054479-A1.
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                                                                                                                                                                                                                                                                                                         ABO28757 standard; protein;
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Human secreted polypeptide I
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RESULT 156
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RESULT 163
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ID ABR94942 standard;
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                                                                                                  Human secreted polypeptide PRO1864, US2003040071-A1.
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                               ADB17071 standard; protein; 234 AA. Human transmembrane PRO polypeptide US2003059462-A1.
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(GETH ) GENENTECH INC
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Human PRO polypeptide #33.
US2003068755-A1.
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                                                         ABM26283 standard; protein;
Human secreted polypeptide;
US2003104549-Al.
05-JUN-2003.
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Human secreted polypeptide E
US2003068722-A1.
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Human secreted polypeptide
US2003064452-A1.
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Human secreted polypeptide PRO1864,
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Human secreted polypeptide I
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(GETH ) GENENTECH INC.
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(GETH) GENENTECH INC.
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                                                                            ABR93112 standard; protein; 234 AA. Human secreted polypeptide PRO1864, US2003064465-A1.
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Human secreted polypeptide
US2003036130-A1.
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           ABR93417 standard; protein;
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Human secreted polypeptide
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Human secreted/transmembrane
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US2003068772-A1.
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                   ABO39484 standard; protein; 234 AA.
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10-APR-2003.
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US2003049771-A1.
13-MAR-2003.
                              ABR86927 standard; protein;
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Human PRO polypeptide #33.
US2003049768-A1.
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Human secreted polypeptide PRO1864,
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US2003068740-A1.
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Human secreted polypeptide PRO1864,
US2003068716-A1.
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Human secreted polypeptide PRO1864,
US2003068692-A1.
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                                                  ABO40704 standard; protein; 234 AA. Human secreted/transmembrane protein
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Human secreted polypeptide PRO1864,
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Human secreted polypeptide 1
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Human secreted polypeptide PR01864,
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US2003054480-A1.
Human secreted p
US2003049740-A1.
13-MAR-2003.
              ABR80544 standard; protein; 234 AA. Human secreted polypeptide PRO1864,
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Human secreted/transmembrane
US2003040074-A1.
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Human secreted/transmembrane
US2003049777-A1.
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US2003049773-A1.
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US2003073179-A1.
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US2003096353-A1.
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Human secreted poly
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Human secreted polypeptide PRO1864,
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ABO29062 standard;
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ABM00545 standard; protein;
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RESULT 282
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Human secreted polypeptide PRO1864,
US2003104557-A1.
05-JUN-2003.
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ABO16602 standard; protein; 234 AA.
Human secreted/transmembrane protein
                                                            US2003092121-A1.
15-MAY-2003.
                                                                              ADA81337 standard; protein; Human secreted/transmembrane
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Human secreted polypeptide |
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US2003054461-A1.
20-MAR-2003
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                                                          ABM13714 standard; protein;
Human secreted polypeptide |
US2003064458-A1.
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US2003032121-A1.
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Human PRO polypeptide #33.
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Best Local Similarity
RESULT 304
ID ABO47760 standard; p
DE Human secreted/trans
PN US2003049747-A1.
PD 13-MAR-2003.
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ID ABO300
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US2003049747-A1.
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Human PRO polypeptide #33.
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US2003049750-A1.
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Human secreted polypeptide PRO1864,
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ABM25368 standard; protein;
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ABR73350 standard; protein;
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RESULT 339
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                                       ABM11274 standard; protein;
Human secreted polypeptide I
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Human secreted polypeptide PRO1864,
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Human secreted polypeptide PRO1864,
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US2003064453-A1.
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Human secreted polypeptide |
US2003068698-A1.
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Human secreted/transmembrane
US2003064468-A1.
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Human secreted polypeptide PRO1864,
US2003068759-A1.
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Human secreted polypeptide PRO1864,
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US2003049754-A1.
                                                                  ABR88147 standard; protein;
Human secreted polypeptide
US2003068720-A1.
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Human secreted polypeptide |
US2003068688-A1.
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ADA00345 standard; protein; 234 AA.
Human secreted/transmembrane polypo
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US2003040072-A1.
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US2003044927-A1.
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US2003044924-A1.
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Human secreted/transmembrane
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                                                              Human secreted polypeptide E US2003073176-A1.
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Human secreted polypeptide I
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US2003064443-A1.
03-APR-2003.
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Human secreted polypeptide
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Human secreted polypeptide PRO1864,
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Human secreted polypeptide PRO1864,
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Human secreted polyI
US2003040067-A1.
27-FEB-2003.
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US2003036151-A1.
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Human secreted/transmembrane protei
US2003036158-A1.
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10-APR-2003.
(GETH ) GENENTECH INC.
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Human secreted polypeptide
US2003054456-A1.
                                     Human secreted/transmembrane US2003068731-A1.
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Human secreted polypeptide |
US2003064450-A1.
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Human secreted polypeptide P
US2003049764-A1.
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Human secreted polypeptide PRO1864, US2003040065-A1.
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(GETH ) GENENTECH INC.
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US2003060600-A1.
27-MAR-2003.
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Mammalian PRO polypeptide (SeqID 14).
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Human secreted/transmembrane PRO
US2003105013<sup>2</sup>A1.
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03-APR-2003.
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Novel human secreted and transmembrane
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                                       ADH24046 standard; protein; 234 AA.
Novel human secreted and transmembrane
US2003180918-A1.
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Novel human secreted and transmembrane
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Novel human secreted and transmembrane
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US2003181707-A1.
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US2003181709-A1.
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         ADI03384 standard;
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Best Local Similarity
RESULT 511
ID AD104779 standard; p.
DE Novel human secreted
PN US2003181657-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC
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ID ADI030
DE Novel
PN US2003
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ID ADH782
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US200318168-A1.
25-SRD-200
 ADI01956 standard; protein; 234 AA.

Novel human secreted and transmembrane protein PRO1864.

US2003181652-A1.

25-SEP-2003.
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Novel human secreted and transmembrane
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Novel human secreted and transmembrane
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Best Local Similarity
RESULT 520
ID ADI03214 standard; p
DE Novel human secreted
PN US2003181655-A1.
PD 25-SEP-2003.
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ID ADI023
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PN US2003
PD 25-SEP
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Human PRO polypeptide #7.
US2003181681-A1.
                  ADH79620 standard; protein; Novel human secreted and tru
US2003191288-A1.
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09-OCT-2003.
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Best Local Similarity
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US2003181678-A1.
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US2003181667-A1.
25-SEP-2003.
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27-FEB-2003.
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25-SEP-2003.
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Novel human secreted and transmembrane
US2003166848-A1.
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Human PRO polypeptide #7.
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Human PRO polypeptide #7.
US2003181637-A1.
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Human PRO polypeptide #33.
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Human PRO polypeptide #7.
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US2003180911-A1.
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Human PRO polypeptide #33.
US2004038337-A1.
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Human PRO polypeptide #31.
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Human PRO polypeptide #7.
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WO2004024076-A2.
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WO2003029423-A2.
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(HYSE-) HYSEQ INC.
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.4e-107;
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.4e-111;
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                                                                                                                 Streptococcus polypeptide SEQ ID NO 9810 WO200234771-A2. 02-MAY-2002.
                             Streptococcus p
WO200234771-A2.
                                                                                                                                                  ABP30317 standard;
                                                                                                                                                                                                                Group B Streptococcus WO200132882-A2.
                                                                                                                                                                                                                                      AAU03699 standard;
                                                                                                                                                                                                                                                         (CNRS) CNRS CENT NAT RECH SCI.
(IFRE-) IFREMER INST FR RECH EXPL MER.
7.8%; Score 93.5;
t Local Similarity 21.9%; Pred. No. 0.
                                                                                                                                                                                                                                                                                                    Putative P. abyssi
FR2792651-A1.
27-OCT-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABB59968 standard; protein; 580 AA. Drosophila melanogaster polypeptide W0200171042-A2.
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                                                  ABP29732 standard; protein;
                                                                                            (CHIR-) CHIRON SPA.
(GENO-) INST GENOMIC RES.
                                                                                                                                                                                           (MICR-) MICROBIAL
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                     )2-MAY-2002
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CHIRON SPA.
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                                       dard; protein; 654 AA.
polypeptide SEQ ID NO 8640.
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polypeptide
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y 25.7%;
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nucleoside-diphosphate-sugar
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sus antigenic
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WO2004058052-A2.
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WO200234771-A2.
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WO2004058052-A2.
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WO2004058052-A2.
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(APPL-) APPLERA CORP.
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infarction-associated
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                                                                                                            AAW13575 standard; protein;
Batten disease polypeptide
W09708308-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADQ39267 standard; protein; 339 AA. Human myocardial infarction-associated WO2004058052-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           JT 647;
ADQ39361 standard; protein; 328 AA.
Human myocardial infarction-associated
WO2004058052-A2.
                         Batten disease CLN3
WO9708308-A1.
06-MAR-1997.
                                                                                                                                                                                          ABU26680 standard;
Protein encoded by
                                                                                                                                                                                                                                                               ADQ39264 standard; protein; 390 AA. Human myocardial infarction-associated
                                                                                                                                                                                                                                                                                                                                                                                               Human NTRAN protein WO2003051902-A1.
                                                                                                                                                                                                                                                                                                                                   Human myocardial
                                                                                                                                                                                                                                                                                                                                                                                                                 ADE28099 standard; protein;
        (GEHO ) GEN HOSPITAL (UYLE-) RIJKSUNIV LEI
                                                                                                                                                                                   WO200277183-A2.
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                                                                                     (GEHO ) GEN HOSPITAL CORF
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Similarity 25.5%;
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infarction-associated
  LEIDEN
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Prokaryotic
                                                    protein;
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7.2%;
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                                                                                                                                                                                                                                                                                                                                               ADQ96392 standard;
T cell activation a
WO2004058805-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Batten disease W09708308-A1.
                                                                                                                                                                                     ADN63244 standard; protein;
Human NOV43a variant.
                                                                                                                                                                                                                                                                                         Human myocardial WO2004058052-A2.
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(ASAH-) ASAHI KASEI PHARMA CORP.

xy Match 7.2%; Score
7.2%; Pred.
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(SHEN/)
            (ANDE/
(ZHON/)
(CATT/)
(JIWW/)
(MILL/)
(MILL/)
(RAST/)
(RAST/)
(STON/)
                                                                          (GORM,
                                                                                                    (PATT/)
(SPYT/)
(EDIN/)
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657
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LL/) MILLET I.
M/) PEYMAN J A.
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CATTERTON E.
JI W.
MILLER C B.
RASTELLI L.
STONE D J.
PENA C E A.
SHENOY S G.
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ANDERSON D
ZHONG M.
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SPYTEK K A.
EDINGER S R.
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MALYANKAR U M.
                                                                          GORMAN L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     standard;
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3 mutant prote
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25.5%;
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25.5%;
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(SPAD/) &
Query Match
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RESULT 6
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RESULT 665
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RESULT 664
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RESULT 662
                                                                                                                                                                     ADQ18055 standard; protein; 473 AA. Human soft tissue sarcoma-upregulat WO2004048938-A2.
                                                        ABB89640 standard;
Human polypeptide
WO200190304-A2.
                                                                                                                        Batten disease CLN3
WO9708308-A1.
                                                  29-NOV-2001
                                                                                                  (GEHO ) GEN HOSPITAL (UYLE-) RIJKSUNIV LEI
                                                                                                                  06-MAR-1997.
                                                                                                                                                                                        (BISE/
                                                                                                                                                                                                                                                                                                                                                                                                                            Human NOV43a.
US2004038223-A1.
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(DIPI/)
(EISE/)
(GANG/)
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Batten disease CLN3 mutant p
                                                                                                                                                                                                                            (SHIM/)
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                                          (HUMA-) HUMAN
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) GANGOLLI E A.
) RIEGER D K.
) SPADERNA S K.
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) GANGOLLI E !
) RIEGER D K.
) SPADERNA S !
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BERGHS C.
DIPIPPO V A.
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RASTELLI L.
STONE D J.
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SHENOY S G.
SHIMKETS R A.
ROTHENBERG M I.
LEACH M D.
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03-OCT-2002.
(ELIT-) ELITRA PHARM 1
                                                                                                                                                                                                                                                         Novel human diagnostic protein #21276. W0200175067-A2. 11-OCT-2001. (HYSE) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                      AAG16921 standard; protein; Arabidopsis thaliana proteir EP1033405-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABU40544 standard;
Protein encoded by
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AAW13586 standard; protein; Batten disease CLN3 mutant pw09708308-A1.
                           ADB85263 standard; protein;
Mouse RNA1 homologue SEQ ID
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Protein encoded by
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Protein encoded by
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WO9708308-A1.
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                                                                                                                                                            AAW13590 standard; protein;
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ry Match 7.2%;
t Local Similarity 26.0%;
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(UYLE-) RIJKSUNIV LEIDEN
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Prokaryotic e
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Prokaryotic essential
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Prokaryotic ess
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21.7%;
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33.7%;
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25.5%;
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20.1%;
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NO:144.
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Pred. No.
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Query Match
Best Local Similarity
RESULT 680
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Human MDDT protein .
WO2003046152-A2.
05-JUN-2003.
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(CAOY/) CAO Y.
(HINK/) HINKLE G.
(SLAT/) SLATER S.
(CHEN/) CHEN X.
                                                                                                                                                                                                                                                                                                                                                                                                             US2003233675-A1.
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ery Match 6.8%;
st Local Similarity 22.6%;
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(GEHO) GEN HOSPITAL CORP.
(UYLE-) RIJKSUNIV LEIDEN.
                          US6610836-B1.
                                           ABO63194 standard;
                                                                                     Arabidopsis thaliana EP1033405-A2.
                                                                                                     AAG53746 standard;
                                                                                                                                        06-SEP-2000.
                                                                                                                                              Arabidopsis thaliana EP1033405-A2.
                                                                                                                                                                AAG25639 standard;
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SYY Match

E Local Similarity 22.6%;
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Human protein sequence SEQ
                                 Klebsiella
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(SLAT/) SLATER S
                                                                                                                                                                                                                                                                                                   (CAOY/) CAO Y.
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Human polypeptide;
WO200153312-A1.
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                                 Human polypeptide WO200153312-A1.
                                                                                 (REAS-) RES ASSOC BIOTECHNOLOGY.
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Protein encoded by
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Vaccinia Virus Major Core pr
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WO200177335-A2.
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ry Match 6.7%;
t Local Similarity 23.3%;
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ry Match 6.7%;
t Local Similarity 19.0%;
                                                                                                                                                      (HYSE-) HYSEQ INC.
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(HUMA-) HUMAN GENOME SCI INC.
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                 HYSEQ INC
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SEQ ID NO
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SEQ ID NO 3097.
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e polypeptide SEQ
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Prokaryotic essential
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Human gene 14 encoded secreted protein
W0200136440-A1.
                  WO200171042-A2.
27-SEP-2001.
                                   ABB58483 standard; protein;
Drosophila melanogaster poly
                                                                                                              AAW27275 standard; protein; 406 AA.
Human cytomegalovirus immediate-early
                                                                                                                                                                                          HCMV IE-exon-4 subunit.
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Human albumin fusion protein
WO200177137-A1.
18-OCT-2001.
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Molasses toxicity
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ry Match 6.7%; Score 79.5;
t Local Similarity 19.3%; Pred. No. 4
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         (PEKE
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18-OCT-2001.
(INCY-) INCYTE GENOMICS INC.
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3ry Match 6.7%;
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                                 Human genome derived single US2003194704-A1.
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Human heart alpha-kinase (HK).
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US2002177205-A1.
                                                                                                                                                                                                                                                                                                                                                                                         ABR58610 standard; protein; 1531 AA.
Human cancer related protein SEQ ID NO:267.
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                                                                                                                                                                                       (RYAZ/) RYAZANOV A.
                                                                                                                                                                                                            JS2002177205-A1.
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                                                                                                                                                                                                                                                                                                       ADE31753 standard; protein; 1531 AA.
Human 59590 protein #SEQ ID 110.
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ry Match 6.6%; S
t Local Similarity 24.3%; F
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                                                                       Novel human protein WO2003025148-A2.
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WO200234771-A2.
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Streptococcus polypeptide SI
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Human diagnostic and therapeutic
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Human TRICH-6, SEQ
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Human diagnostic WO2004023973-A2.
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AAE21170 standard; protein;
Human TRICH-14 protein.
WO200212340-A2.
                                                                           ABB98345 standard; protein;
Human ABC transporter ABCB9
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Amino acid sequence of a human TAP-like
WO200173018-A2.
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Human cancer associ
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WO200164875-A2.
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                                                   (ACTI-) ACTIVE PASS
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WO200177335-A2.
18-OCT-2001.
(INSP ) INST PASTRIP
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EP1033405-A2.
06-SEP-2000
                                                Polypeptide encoded WO2003023013-A2.
                                                                 ABO00771 standard;
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Protein encoded by
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                                                                                                  (HYSE-) HYSEQ INC.
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(GEHO ) GEN HOSPITAL CORP.
(UYLE-) RIJKSUNIV LEIDEN.
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Mouse melatonin la
US6326526-B1.
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Variola smallpox virus AlOL.
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Mouse Batten disease polypeptide
WO9708308-A1.
                               ADM25403 standard; protein; 383 AA
Hyperthermophile Methanopyrus kand
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Mouse GPCR MTNR1A;
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SEQ ID NO:655.
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EP1033405-A2.
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EP1033405-A2.
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T cell activation associated protein
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ery Match 6.4%;
21.8%;
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Human 164-1b protein (SeqID
WO2003097686-A1.
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WO2003097686-A1.
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HCV antigen T7N1-30.
EP518313-A2.
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Klebsiella pneumoniae polypeptide s
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Human cytoskeleton-associated protein (CSAP)-3 WO200242330-A2.
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Human hypothetical
WO2004061123-A2.
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EP1033405-A2.
                                                                                                                                                                                                                                                                                                Arabidopsis thaliana
EP1033405-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              H. pylori transporter protein, WO9640893-A1.
ABB89424 standard; protein; 456 AA.
Human polypeptide SEQ ID NO 1800.
                                                                               ADQ96246 standard;
T cell activation a
                                                                                                                                                                                                                06-SEP-2000.
                                                                                                                                                                                                                                             AAG09591 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADN21126 standard; protein; 2539 AA.
Bacterial polypeptide #3779.
US2003233675-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAW20918 standard;
                                                  15-JUL-2004.
(ASAH-) ASAHI KASEI PHARMA CORP.
                                                                       WO2004058805-A2.
                                                                                                                                15-JUL-2004.
(ASAH-) ASAHI KASEI PHARMA CORP.
                                                                                                                                                       WO2004058805-A2.
                                                                                                                                                                                                                                                                                                                   AAG09592 standard; protein; 274 AA.
                                                                                                                                                                                                                                                                                                                                                           (DOUC/) DOUCETTE-STAMM L A. (BUSH/) BUSH D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     GOLD/) GOLDMAN B S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SLAT/) SLATER S C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (NISC-) JAPAN SCI & TECHNOLOGY CORP.

CY Match 6.4%; Score 76.

Local Similarity 22.6%; Pred. No.
                                                                                                           Local Similarity
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                                                                                                                                                              ; protein; 366 AA.
associated protein #211.
                                                                              protein; 366 AA. associated protein
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                                                                                                                                                                                                                                             protein; 287 AA.
                                                                                                                                                                                                                                                                                                                                                                                                             protein; 195 AA
                             6.4%;
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22.0%;
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26.7%;
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26.7%;
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25.9%;
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22.1%;
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19.2%;
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                              Score
Pred.
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No. 18;
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11;
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Best Local Similarity RESULT 789
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RESULT 786
                                                                                                                          Query Match
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(HINK/) HINKLE G J.
(SLAT/) SLATER S C.
(CHEN/) CHEN X.
                                                                      ADM92206 standard; protein; 263 AA. S pneumoniae antigenic protein sequence WO2004020609-A2.
                                                                                                                                                                                                                                     ABB63150 standard; protein; Drosophila melanogaster polyw0200171042-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAB53400 standard; protein; 557 AA. Human colon cancer antigen protein WO200055351-A1.
                                                                                                                                             US6699703-B1.
02-MAR-2004.
                                                                                                                                                              ADK46633 standard; protein;
Streptococcus pneumoniae pro
                                                                                                                                                                                                                           27-SEP-2001
                                                                                                                                                                                                                                                                                                                                                               ADN23383 standard; protein; 1917 AA.
Bacterial polypeptide #6036.
US2003233675-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADN22849 standard; protein; Bacterial polypeptide #5502. US2003233675-A1.
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            AAY81619 standard;
                                                                                                                                                                                                                    (PEKE )
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAY44945 standard; protein;
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                                                    (TUFT ) UNIV TUFTS.
                                                              L1-MAR-2004.
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(SLAT/) SLATER S
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h 6.3%; Score
Similarity 18.0%; Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DU PONT DE NEMOURS & CO E I.
h 6.4%; Score 76;
Similarity 21.4%; Pred. No.
                                Similarity
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dard; protein;
pneumoniae typ
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6.4%;
22.0%;
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18.5%;
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polypeptide
                                                                                                                                                                 in; 263 AA.
protein, Seq
  type
  264
Pe 4
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                                          263;
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RESULT
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Novel S. pneumoniae protein s
US6800744-B1.
05-OCT-2004.
(GENO-) GENOME THERAPEUTICS C
uery Match
est Local Similarity 18.0%;
                                                          __acterial polypeptide #13272.
US2003233675-A1.
                                                                                                                                       AAU03852 standard;
G protein-coupled 1
WO200138533-A2.
                        (CAOY/) CAO Y.
(HINK/) HINKLE G G
(SLAT/) SLATER S G
(CHEN/) CHEN X.
                                                                                                                                                                                                            G protein-coupled WO200138533-A2.
                                                                                                                                                                                                                                                                                        ADH51470 standard; protein; Rat MT1 receptor amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     S. pneumoniae type WO200277021-A2.
                                                                                                                                                                                                                                                                                 FR2835847-A1.
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                                                                                                                                                                          (PHAA ) PHARMACIA & UPJOHN.
ry Match 6.3%;
t Local Similarity 19.1%;
                                                                                                                                                                                                                              AAU03851 standard;
                                                                                                                                                                                                                                                                                                                 (ELIT-) ELITRA PHARM INC.
(ELIT-) 6.3%;
ry Match 6.3%;
t Local Similarity 31.7%;
                                                                                                                                                                                                                                                                                                                                                     E. coli proliferation WO200044906-A2.
                                                                                                                                                                                                                                                                                                                                                                    AAB15936 standard;
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ry Match 6.3%;
Local Similarity 23.5%;
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(GENO-) INST GENOMIC RES.
                                                                                                     Local Similarity
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Similarity
                 GOLDMAN B
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BAX-associated |
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              Ġ
                                                                                                                                                                                                                     ; protein; 397
receptor-like
                                                                                                                                                protein; 433 receptor-like
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e protein sequence,
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4 strain protein
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6.3%;
19.1%;
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6.3%;
21.9%;
6.3%;
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Score
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1 sequence
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Score
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d protein
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(GPCR-like)
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(GPCR-like)
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No. 17;
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RESULT 799
ID ADO295
DB Mouse (
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RESULT
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RESULT 806
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RESULT 800
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13-652958-B1.
13-637-2003.
                                            Enterococcus 1
US6617156-B1.
                                                                                                                 Human transporter WO2004048599-A2.
                                                                                                                                                                                        Human NF-kappaB
WO2004065577-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                   AAU45917 standard; protein; Propionibacterium acnes imm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADM72132 standard; protein; 392
Human NTRAN polypeptide (clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      G protein-coupled WO200138533-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mouse GPCR HTR2A
WO2004040000-A2.
                                                                                                                                   ADP99138 standard;
                                                                                                                                                                                 05-AUG-2004.
                                                                                                                                                                                                                                                                                                                                                       ABM42436 standard;
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                                                              ADH86490 standard;
                                                                                                         10-JUN-2004.
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                                                                                                                                                                                                           ADR14597 standard;
                 BUSH/) BUSH D.
                                                                                                                                                                                                                                                                                                                                                                                          (CORI-)
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h 6.3%;
Similarity 19.1%;
Similarity
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                                                                                                INCYTE CORP
                           DOUCETTE-STAMM L
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CR HTR2A, S
                                                  ndard; protein;
faecalis polype
                                                                                                                                                                                                rd; protein; 473 AA.
pathway-associated
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                                                                                                                         ; protein; 480 AA. and ion channel (
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6.3%;
18.7%;
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21.0%;
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predicted C
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18;
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Seven transmembrane WO9412635-A2.
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Antagonist of cell
                  AAR53748 standard; protein; 355 AA
Seven transmembrane receptor (V28)
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(MATE-) INST MATERIALS RES & ENG.
(MATE-) INST MATERIALS RES & ENG.
(YOUR STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STAN
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                                                                                                                                                                        Rat 164-1h protein
WO2003097686-A1.
                                                                                                                                                                                                                    ADF74954 standard;
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ry Match 6.3%; Score 75; DB 8; Le
Local Similarity 22.9%; Pred. No. 1.8e+02;
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(REAS-) RES ASSOC BIOTECHNOLOGY.
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JP06141870-A.
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hepatitis virus
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                                                                                                                                                                                           protein; 25 (SeqID 13).
                                                                                  IND LTD.
6.2%;
23.3%;
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22.9%;
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22.9%;
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polypeptide
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62;
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1.8e+02;
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Query Match: Part Local Similarity RESULT 817
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RESULT 819
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(IPFP-) IPF PHARM GMI
(FORS/) FORSSMANN U.
.....ard; protein;
Transmembrane domain
US6348574-B1.
                                                                                         T 824
AAU91235 standard, protein, 355 AA.
Thransmembrane domain receptor
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23-AUG-2001.
(MILL-) MILLENNIUM PHARM INC
                                                                                                                                                                              AAB82786 standard; pi
Human CX3C chemokine
                                                                                                                                                                                                                                                         Human CX3CR1 protein.
WO200172830-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                Human 7TM receptor US6107475-A.
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Human G protein-coupled receptor
W0200022129-A1.
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Human mutant G prol
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                                                                                   US6348574-B1.
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                                                                CORP.
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G protein-coupled receptor
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V28 cDNA
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V28 cDNA
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ne receptor 1.
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6.2%;
25.8%;
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27-MAR-2003.
(EOSB-) EOS BIOTECHNOLOGY INC.
                                                                                                                                                              ADC22649 standard; protein; 355 AA.

Human G protein-coupled receptor (GPCR)
US655339-B1.
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Human fractalkine i
WO2003039475-A2.
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                                                                      US2003105292-A1.
05-JUN-2003.
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ADH14224 standard; protein;
ADH14224 standard; protein;
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(AREN-) ARENA PHARM INC.
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07-FEB-2002.
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(LIFE-) LIFESPAN BIOSCIENCES INC.
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(TOPI-) TOPIGEN PHARM INC.
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                                                  LIAW/) LIAW C W.
BEHA/) BEHAN D P.
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US2003105292-A1.
05-JUN-2003.
(LIAW/) LIAW C W.
                                                                                                                 ADQ39421 standard; protein; 355 AA. Human myocardial infarction-associated W02004058052-A2.
                                                                                                                                                                                     ADP23931 standard; protein; 355 PRO polypeptide SEQ ID NO:1109. WO2004041170-A2. 21-MAY-2004.
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Human PRO protein sequence 9
WO2004039956-A2.
13-MAY-2004.
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                                     ADQ39422 standard; protein; 362 AA. Human myocardial infarction-associated WO2004058052-A2.
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Human GPCR CX3CR1,
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WO2003104484-A1.
                                                                                               (APPL-) APPLERA CORP.
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(BEHA/) BEHAN D P.
(CHAL/) CHALMERS I
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                   APPLERA CORP.
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SEQ ID NO:1996
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                                                  Human protein; encoded by a f EP1396543-A2.
             10-MAR-2004.

(REAS-) RES ASSOC BIOTECHNOLOGY.

17 Match
6.2%; Scc
17 Match
23.1%; Pro
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Human polypeptide,
EP1130094-A2.
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Rat 164-1b protein
WO2003097686-A1.
                                                                                                                                                                                                                                                                                                            Rat 5-HT2 receptor
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Rat 5-HT2A serotonin receptor C3
WO9838217-A1
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ry Match 6.2%;
t Local Similarity 23.3%;
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Rat 5-HT2A serotonin receptor
ADQ96138 standard; protein; 562 AA
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Rat 5-HT2A serotonin
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(EGAN/) EGAN C C.
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(HERR/) HERRICK-DAVIS
(EGAN/) EGAN C C.
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(EGAN/) EGAN C C.
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(HERR/) HERRICK-DAVIS
(EGAN/) EGAN C C.
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SEQ ID NO: 3602.
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in receptor C322E
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receptor C322R mutant
                                                                                                                                                                                                                                                                                                                                                                                                             receptor.
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full length
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or C322K
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Pred. No. 23;
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Pred. No. 23;
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                  Score 74.5;
Pred. No. 3
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Best Local
RESULT 853
                                                                                                                                                           Query Match
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                                    Human adipocyte WO200286122-A2.
                                                                                                                                                                            US6605709-B1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADR86160 standard; protein; 587 Aspergillus fumigatus essential WO2004067709-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    T cell activation WO2004058805-A2.
                                             ABU70366 standard; protein;
Human adipocyte bait proteir
                                                                                                             Human adipocyte WO200286122-A2.
                                                                                                                                                                                                                                              (MOLE-) INST MOLECULAR & CELL BIOLOGY.
                                                                                                                                                                                                                                                                                  AAE20477 standard;
HCV-S1 full-length
                                                                                                                                                                                                                                                                                                                                  (FARB ) BAYER AG
                                                                                                                                                                                                                                                                                                                                                    Herbicidally active WO200210210-A2
                                                                                                                                                                                                                                                                                                                                                                                                                    Acinetobacter baumannii
US6562958-B1.
13-MAY-2003.
                                                                                                                                                                                                                                                                                                                                                                                                                                               ADA36878 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Drosophila melanogaster polypeptide WO200171042-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABB62948 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (ELIT-) ELITRA CANADA LTD.

ry Match
t Local Similarity 18.2%;
                                                                                                                                 ABU70365 standard;
                                                                                                                                                                                                                                                                  31-JAN-2002
                                                                                                                                                                                                                                                                                                                                            07-FEB-2002
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                                                                                             (HYBR-)
                                                                                                                                                                                                                                                                            WO200208447-A2.
                                                                                                                                                                                                                                                                                                                                                                                                            (GENO-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (PEKE ) PE CORP NY
                   (HYBR-)
                                                                                                                                                                      (GENO-)
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                                                                        Local Similarity
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Similarity
                   HYBRIGENICS
                                                                                           HYBRIGENICS.
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s bait protein.
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6.2%;
23.1%;
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26.4%;
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polypeptide SEQ ID NO
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23.8%;
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17.3%;
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27.2%;
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Pred. No.
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#4039.
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gene
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No. 1.
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No. 32;
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No. 30;
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No. 32;
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No. 3e+02;
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5.6;
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(JCRP-) (
Query Match
Best Local s
RESULT 868
ID ABP81'
DE Hum'
PN W'
PD
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Best Local Si
RESULT 866
ID AAW15786 :
DE Melatonin
PN JP0908458;
PD 31-MAR-19;
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ID ADR940
DE Novel
PN US6800
PD 05-OCT
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(GENO-) INST GENOMIC
Query Match
Best Local Similarity
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12-OCT-2001.
(INRG ) INRA I
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(MASS-) MASSACHUSETTS GEN HOSPITAL.
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(MASS-) MASSACHUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAR88412 standard; protein;
High-affinity melatonin-la
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(SLAT/) SLATER S C.
(CHEN/) CHEN X.
(GOLD/) GOLDMAN B S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacterial polypeptide #22913. US2003233675-A1.
                               ABP81840 standard; protein; 350 AA. Human melatonin receptor type 1a protein WO200261087-A2.
                                                                                                                                                                                                 AAW94761 standard; protein; 350 i
Human melatonin receptor protein
                                                                                                                                                                                                                                                                                                                                     Melatonin receptor JP09084581-A.
                                                                                                                                                                                                                                                                                                                                                   AAW15786 standard; protein;
Melatonin receptor protein.
                                                                                                                                                                                   EP892046-A2.
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Novel S. pneumoniae protein
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WO200277021-A2.
                                                                                                                                          20-JAN-1999.
(JCRP-) JCR PHARM
                                                                                                                                                                                                                                                                                                31-MAR-1997.
(TAKE ) TAKEDA CHEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO9535320-A1.
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(HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel human polypeptide WO2003023013-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABO00448 standard;
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6.2%;
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US6800744-B1.
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h 6.2%; Score 74;
Similarity 24.3%; Pred. No.
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ptide #35.
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6.2%;
18.5%;
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6.2%;
24.3%;
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18.5%;
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24.3%;
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38.3%;
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21.2%;
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yiiG.
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sequence,
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n mel-la.
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RESULT 876
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Human GPCR MTNR1A,
WC2004040000-A2.
                                               AAR54067 standard; protein; Non-A, non-B hepatitis virus JP06141870-A.
                                                                                                                05-JUL-2001.
(SAOC) MERCIAN CORP.
                                                                                                                                   Flavobacterium lutescens L-lysine-6-aminotransferase \mathtt{W}0200148216\text{-Al}.
                                                                                                                                                                                                               AAY80509 standard; protein; 492 AA. F. lutescens L-lysine:2-oxoglutarate WO200008170-A1.
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Rat growth hormone
WO9721730-A1.
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FR2807446-A1.
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                                                                                                                                                       AAG64105 standard; protein;
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secretagogue receptor
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PN JP0713
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Arabidopsis thaliana p
SP1033405-A2.
06-SEP-2000.
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Protein encoded by I
WO200277183-A2.
03-OCT-2002.
                                               Codon optimised hCMV IE1 encoded W02004058166-A2.
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12-AUG-2003.

(GENO-) GENOME THERAPEUTICS

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17.4%;
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5'UTR/CORE/ENV/NS1
JP07133291-A.
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      AAG51385 standard; protein;
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                               Candida albicans
WO200253728-A2.
                                                                                             ADQ75725 standard; Wild type hCMV IE1. WO2004058166-A2.
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Protein encoded by
WO2004042346-A2.
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WO2004042346-A2.
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WO200163286-A2.
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WO2004042346-A2.
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Protein encoded by
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Query Match
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RESULT 897
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ID AB
DB Dr
PN WO
PD 27
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ABP29367 standard; protein; 249 Streptococcus polypeptide SEQ II WO200234771-A2. 02-MAY-2002.
                                                                                                                                                          Human G protein-coupled receptor from WO200177330-A2.
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(HINK/) HINKLE G :
(SLAT/) SLATER S (
(CHEN/) CHEN X.
                                                                                      E. faecium protein US6583275-B1.
                                                                                                                                                                                                                                                                                                                        AAR33214 standard;
NANBH virus strain
EP532167-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABG29128 standard; protein; Novel human diagnostic prote WO200175067-A2.
                                                                                                                                                                                                                                                                                                                                                                                                    Drosophila melanogaster protein, WO2004039999-A2.
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Bacterial polypeptide #17311.
US2003233675-A1.
18-DEC-2003.
                                              (GENO-) GENOME THERAPEUTICS ry Match 6.1%; t Local Similarity 22.6%;
                                                                                                         ADC97146 standard;
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(ASTR ) ASTRA AB.
                                                                                                                                                                                                                                                    H. pylori secreted
                                                                                                                                                                                                                                                                                                                                                                                                                        ADS96670 standard; protein; 1287 AA
                                                                             24-JUN-2003
                                                                                                                          (PHAA ) PHARMACIA & UPJOHN CO.

ry Match 6.1%; Score
Local Similarity 20.3%; Pred.
                                                                                                                                                                                                                                            WO9640893-A1.
                                                                                                                                                                                                                                                                AAW20571 standard;
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ry Match 6.2%; Score
Local Similarity 18.2%; Pred.
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                                                                                                                   Local Similarity 903
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                                                                                              protein; 199 AA.
sequence SEQ ID
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27.4%;
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protein #29119.
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polypeptide SEQ
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16-JAN-2003.
                                                                                                                                                                                                                                                                                                                    Breast cancer associated
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADH80191 standard; protein;
Fungal 7091 elongase proteir
                                                                                                                                                                                                                                                                ADN61865 standard; protein;
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WO200208401-A2.
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ry Match 6.1%;
t Local Similarity 20.6%;
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(LEON/) EUN-YEONG LEONARD
(HUAN/) HUANG Y.
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KEKUDA R.
PATTURAJAN M.
GANGOLLI E A.
VERNET C A M.
GUO X S.
TCHERNEV V T.
ALSOBROOK J P.
LEPLEY D M.
RIEGER D K.
                       CATTERTON E.
LEITE M W.
ZHONG H.
                                               ANDERSON D I
SPADERNA S I
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SPYTEK K A.
SHENOY S G.
TAUPIER R J.
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GERLACH V.
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CASMAN S J.
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protein #2394
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TELO1 from plasmid
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RESULT

919

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Query Match
Best Local Similarity
RESULT 910
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                                                                                 AAG24012 standard; protein; 4
Arabidopsis thaliana protein
EP1033405-A2.
06-SEP-2000.
                                                                                                                                           Arabidopsis thaliana EP1033405-A2. 06-SEP-2000.
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Rat growth hormone
WO200132705-A1.
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                                 Protein encoded WO200277183-A2.
                                         ABU31419 standard;
Protein encoded by
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Staphylococcus aureus protein of
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ry Match 6.1%;
t Local Similarity 19.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A mouse growth hormone WO200002918-A1.
                                                                                                                                                                    AAG24013 standard;
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NE BEECHAM PLC.

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secretagogue
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Prokaryotic
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ID NO:125.
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Best Local Similarity
RESULT 928
ID ADQ96000 standard;
DE T cell activation a
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(CNRS) CNRS CENT NAT RECH S
PRY Match
6.1%;
24.6%;
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EP1033405-A2.
                                          06-SEP-2000.
                                                  Arabidopsis t.
EP1033405-A2.
                                                                                                                                                                                                  ADH42229 standard; protein; Novel human protein NOV50d.
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Human NOV13b protein SEQ ID
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ADQ96000 standard; protein; 608 AA.
T cell activation associated protein #89.
                                                                     AAG24011 standard;
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24-JUL-1997.
24-JUL-1997.
(SMIK) SMITHKLINE BEECHAM P.
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ery Match 6.1%;
23.3%;
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27-SEP-2001.
(PEKE) PE CORP NY.
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(ASAH-) ASAHI KASEI PHARMA CORP.

EXY Match

Cimilarity 19.5%; Pre
ABJ19057 standard; protein; 792 AP
Pathogen specific antigen related
                                                                     AAU36734 standard; protein; 792
Staphylococcus aureus cellular p
                                                                                                                                    Protein encoded WO200277183-A2.
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Protein encoded by
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                                                                                                                                                                                                                                                                               Human adult neural WO9857976-A1.
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(SMIK ) SMITHKLINE BEECHAM
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                                             (ELIT-) ELITRA
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Prokaryotic esse
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EP1394274-A2.
03-MAR-2004.
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Protein encoded by
WO9825960-Al.
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(CIST-) CISTEM BIOTECHNOLOGIES
                                                                           ABG05866 standard; protein; Novel human diagnostic prote WO200175067-A2.
                                                                                                                                                                 ADJ76159 standard; protein;
Marker gene related amino ac
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                                                                                                                                                                                                                                                      ABB07819 standard; protein; 966 Mouse polycystic kidney disease
                                                                                                                                                                                                                                                                                   (MILL-) MILLENIUM PHARM INC.
xy Match 6.1%;
t Local Similarity 21.3%;
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Human protein similar to yeast
WO2004078035-A2.
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                   ADR99135 standard;
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h 6.1%; Score 73; DB
Similarity 26.2%; Pred. No. 78;
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Best Local Similarity
RESULT 948
ID ABUREA
 Best Local Similarity
RESULT 955
ID AAW23832 standard;
DE Human oxytocin rece
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity RESULT 947
                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity RESULT 951
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                                                                 AAR37264 standard; p
Oxytocin receptor.
EP542424-A1.
19-MAY-1993.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABU15302 standard; I
Protein encoded by I
WO200277183-A2.
03-OCT-2002.
                                                                                                                                                                                                                                                                            Enterococcus faecalis polypeptid US6617156-B1
                                                                                                                                                                         Enterococcus faecalis polypeptide #2037.
US6617156-Bl.
                                                                                                                                                                                                                                                                                                                                                                            ABB53675 standard; protein; 325 AA. Lactococcus lactis protein ydhB. FR2807446-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABG07373. standard; protein; 976 AA. Novel human diagnostic protein #7364. W02001,75067-A2.
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(FARB ) BAYER PHARM
AAW23832 standard; protein;
Human oxytocin receptor.
                                                                                                                                                                                                                                                                                                                                (INRG) INRA INST NAT RECH AGRONOMIQUE.

EXY Match 6.1%; Score 72.5;

L Local Similarity 25.9%; Pred. No. 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABB53879 standard;
Lactococcus lactis
FR2807446-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABU05456 standard; protein; 209 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                        (INRG ) INRA INST NAT RECH AGRONOMIQUE.

ry Match 6.1%; Score 72.5;

t Local Similarity 22.9%; Pred. No. 22;
                                                                                                                                                                                                                                                   (DOUC/) DOUCETTE-STAMM L A. (BUSH/) BUSH D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (ELIT-) ELITRA PHARM INC.
(ELIT-) ELITRA PHARM INC.
6.1%;
C Local Similarity 20.5%;
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                                                       ROHT ) ROHTO PHARM
                                                                                                                                              BUSH/) BUSH D.
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                                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                         ocal Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                protein; 307 AA protein yfgG.
                                                                                                   protein;
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Prokaryotic (
                                4 CO LTD.
6.1%;
24.5%;
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6.1%;
19.5%;
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25.0%;
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21.5%;
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22.1%;
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19.5%;
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             389
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Pred.
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No. 27;
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No. 31;
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Best Local Similarity
RESULT 963
ID AAR58663 standard, p
DE Bovine PACAP recepto
PN EP618291-A2.
          Best Loc
RESULT 964
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RESULT 957
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human oxytocin receptor protein. W02003664402-Al.
                                                                                                                                       AAR58665 standard; protein; 448 AA.
Bovine PACAP receptor type 1B matur
EP618291-A2.
                                                                                                                                                                                                                                                                                                          Human oxytocin receptor poly WO2004000993-A2.
                                                                                                                                                                                                                       ADO29590 standard; protein; 389 AA. Human GPCR OXTR, SEQ ID NO:692. WO2004040000-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABP81865 standard; proto
Human oxytocin receptor
WO200261087-A2.
                                                                                                 (TAKE ) TAKEDA CHEM IND LTD.
xy Match 6.1%;
t Local Similarity 29.6%;
                                                                                                                                                                                                                                                             OZOUTETTIAN ONTREAL.
(UYOU-) UNIV QUEBEC A MONTREAL.
(UYMO-) UNIV MONTREAL CENT HOSPITALIER.
(UYMO-) UNIV MONTREAL CENT HOSPITALIER.
6.1%; Score 72.5;
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AAR58657 standard; protein; 485
                                                                                                                                                                                                     (PRIM-) PRIMAL INC.
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ry Match 6.1%; 
t Local Similarity 24.5%;
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                    Local Similarity
                                       TAKEDA CHEM IND LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   seQ ID NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein; 389 eptor protein
                   6.1%;
29.6%;
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24.5%;
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24.5%;
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24.5%;
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polypeptide
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3362.
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Best Local Similarity
RESULT 970
ID ABU25159 standard; p
DE Protein encoded by P
N W0200277183-A2.
PD 03-0CT-2002.
PA (ELIT-) ELITRA PHARM
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Best Local S
RESULT 966
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Best I
RESULT :
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Best Loca
RESULT 967
                          Best
RESULT
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20-DEC-2001.
(REGC) UNIV CALIFORNIA.
(REGC) 6.1%;
Match 6.1%;
22.3%;
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ADQ96378 standard; T cell activation a WO2004058805-A2.
                                                                                                                                                                                                                                                                                          ABB05429 standard; protein; Arabidopsis thaliana ABH1 pu WO200196585-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EP618291-A2.
05-OCT-1994.
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Bovine PACAP receptor type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                05-OCT-1994
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                                                                                AAR34580 standard; protein;
Human hepatitis C virus gene
                                                                                                                                                                                                                   Arabidopsis thaliana WO200281696-A2.
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ry Match 6.1%;
t Local Similarity 29.6%;
                                                                                                                                                                                                                                                                                                                                               (ROOS/) ROOS J.
(STAU/) STAUDERMAN
(VELI/) VELICELEBI
                                                                                                                                                                                                                                                                                                                                                                                  C. elegans protein
US2004009537-Al.
                                                                                                                                                                                                                                     AAE31528 standard;
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(GOLD/) GOLDMAN B
                                                                                                                            (ELIT-) ELITRA PHARM
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(SLAT/) SLATER S
                           Local Similarity
972
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h 6.1%; Score
Similarity 22.3%; Pred.
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                                                    KAGAKU
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        ; protein; 208 AA. associated protein #278.
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                                                                                                                                                      protein; 851 AA.
Prokaryotic esse
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6.1%;
20.5%;
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6.1%;
29.6%;
                                   KENKYUSHO CO.
6.1%; Score 72.
23.7%; Pred. No.
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20.2%;
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22.5%;
                                                                                                                                                                                                                            protein
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protein S
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No. 42
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No.
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No.
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No. 45;
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No
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90;
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79;
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91;
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90;
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Query Match
Best Local Similarity
RESULT 973
ID ABB48543 standard; I
DE Listeria monocytoger
PN W0200177355-A2.
PD 18-OCT-2001
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Best Local S
RESULT 974
ID ABU39432 a
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RESULT 980
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                                               RESULT 981
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                                                                                                                                                                                                     ABU19932 standard; protein encoded by WO200277183-A2. 03-OCT-2002.
                 Arabidopsis thaliana protein EP1033405-A2.
                                                                         Arabidopsis thaliana protein; BP1033405-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABB48543 standard; protein;
Listeria monocytogenes prote
WO200177335-A2.
                                                                                                                                                                                                                                                                                                                                                                                                             Human colon cancer WO200055351-A1.
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Protein encoded by
                                                                                                                                                                                                                                                                                                                                                       Human G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO200277183-A2.
                                                                        06-SEP-2000.
                                                                                                                                (HYSE-) HYSEQ
                                                                                                                                               ABG25051 standard; protein; Novel human diagnostic protw0200175067-A2.
                                                                                                                                                                                              (ELIT-) ELITRA PHARM
                                                                                                                                                                                                                                                                                                                                                Human G coupled-protein receptor, WO200017641-A1.
                                                                                                                                                                                                                                                                                                                                                                AAY87505 standard;
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WO200277183-A2.
                                                                                                                                                                  Arabidopsis thaliana
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T cell activation a
WO2004058805-A2.
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Human GPCR XPR1 protein SEQ
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Tumour-associated a
WO2003024392-A2.
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EP1033405-A2.
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Protein encoded by
                                  Photorhabdus luminescens WO200294867-A2.
28-NOV-2002.
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WO200075335-A2.
                                              Arabidopsis thaliana EP1033405-A2.
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Recombinant fusion
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(BODA-) BODAO GENE
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                                                                                                                                                                                                                                                                                                                                         (AGOU-) AGOURON PHARM INC
                                                                                                                                                                                                                                                                                                                                                 17-FEB-2000
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h 6.0%;
Similarity 23.6%;
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6.0%; Score 72;
26.3%; Pred. No.
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pHCAP-1 polyprotein.
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protein;
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23.6%;
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polypeptide
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full
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se protein
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Query Match
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RESULT 1014
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US2003150017-A1.
07-AUG-2003.
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W09535320-A1.
                                               ABP58069 standard; protein;
Human G-protein coupled rece
                                                                                                                  Angiogenesis-associated human WO200279492-A2.
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US2004161823-A1.
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                                                                                                                                                        (MASS-) MASSACHUSETTS GEN HOSPITAL.
ry Match 6.0%; Score
t Local Similarity 23.1%; Pred.
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(MINT/) MINTIER G.
(RAMA/) RAMANATHAN
                                                                                                                                                                                                                                                                                                                             ADR40542 standard; protein;
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(GRAH/) GRAHAM M W.
(FAIR/) FAIRBAIRN D
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AVENTIS PHARM INC.
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Similarity 22.3%;
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6.0%; Score
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h 6.0%; Score 71.5
Similarity 26.5%; Pred. No.
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ita plk1 p
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                                               receptor GAVE1
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protein.
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Human EDG-1 protein.
US2002155512-A1.
24-OCT-2002.
                                       ADJ45541 standard; g
LXR-ligand induced t
U82004023276-A1.
05-PEB-2004.
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Human endothelial
WO2003029277-A2.
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Human Edg1 receptor.
WO2003006503-A1.
                                                                                                                             ABM85457 standard; protein; 382 AA. Human protein sequence hCP1630135. WO2003073826-A2.
                                                                                                                                                                                                              ADN38684 standard; protein; 382 AA. Cancer/angiogenesis/fibrosis-related polypeptide, WO2003042661-A2.
                                                                                                                                                                                                                                                                                                        ADC40477 standard; protein; Protein of human EDG-1.
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Human sphingolipid
WO200261087-A2.
                                                                                                                                                                                                                                                     (TAKE ) TAKEDA CHEM IND LTD.
ry Match 6.0%;
t Local Similarity 22.3%;
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Human EDG1, SEQ ID
WO2003072824-A1.
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ry Match 6.0%; 
t Local Similarity 22.3%;
                                                                                      (SAGR-) SAGRES DISCOVERY.
(SAGR-) 6.0%;
ry Match 6.0%;
t Local Similarity 22.3%;
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LINSLEY P
LUND E.
                             WARD T R.
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differentiation sphingolipid
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transcript
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                                                                                                                                                                                                                                                                                                                                                          Rat vesicle membrane protein; 394 AA. US2003175787-A1.
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                                                               ABU26033 standard;
Protein encoded by
WO200277183-A2
                                                                                                                                               ABP75877 standard; protein;
Human secretory polypeptide
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                                                                                                                              WO200283876-A2.
24-OCT-2002.
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WO200177335-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                        (FARB ) BAYER AG.
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ry Match 6.0%;
t Local Similarity 22.3%;
ABJ37074 standard; protein; 565 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (CAOY/) CAO Y.
                                                                                                                                                                                               ) UNIV CALIFORNIA.
                                                                                                   INCYTE GENOMICS INC.
h 6.0%;
Similarity 22.4%;
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                                             ELITRA PHARM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                standard; protein;
polypeptide #2267
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Prokaryotic e
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                               4 INC.
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22.7%;
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protein #727
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1 protein
                                                                                                                                                                                                                        in; 441
Region
                                                                                                                                                470 AA.
SPTM SEQ
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Pred.
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sequence
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                            71.5; 1
No. 61;
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No. 47;
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No. 39;
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                                     524;
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Query Match
Best Local f
RESULT 1038
ID ABM72
DE Star
PN W
                                                                     RESULT 1042
ID ABG0088
DE Novel h
PN W020017
PD 11-0CT-
                             Query Match
Best Local Similarity
RESULT 1043
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Best Local Similarity
RESULT 1041
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                                                                                                                                                                 AAB07591 standard; protein; A human methionine synthase WO200042196-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Staphylococcus aureus WO200294868-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABU16392 standard; protein; 603 AA.
Protein encoded by Prokaryotic essential
W0200277183-A2.
03-OCT-2002.
(ELIT-) ELITEA PHARM INC.
EXP MAICH
6.0%; Score 71.5;
Local Similarity 21.3%; Pred. No. 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAW51244 standard;
Human calcitonin re
WO9821242-A1.
                                                                              ABG00883 standard; protein; Novel human diagnostic prote W0200175067-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO2003000012-A2
ADM43211 standard; protein; 698 AA. Human methionine synthase reductase US2003082676-A1.
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Human methionine synthase re
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABM72619 standard;
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(HUMA-) HUMAN GENOME
                                                          (HYSE-) HYSEQ INC.
                                                                                                                                           20-JUL-2000.
(UYMC-) UNIV MCGILL.
                                                                                                                                                                                                                                                                                                   Human methionine synthase reductase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (MILL-) MILLENNIUM PHARM INC.
                                                                                                                                                                                                                            (WILS/) WILSON A.
(ROSE/) ROSENBLATT D.
                                                                                                                                                                                                                                                 (GRAV/) GRAVEL R A. (ROZE/) ROZEN R. (LECL/) LECLERC D.
                                                                                                                                                                                                                                                                                           US2003082676-A1.
                                                                                                                                                                                                                                                                                                              ADM43217 standard; protein;
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                                                                                                                                                                                                                                                                                                                                                                         (GRAV/) GRAVEL R A. (ROZE/) ROZEN R. (LECL/) LECLERC D.
                                                                                                                                                                                                                                                                                                                                                                                                                    JS2003082676-A1.
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                                                                                                                        Local Similarity
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22.8%;
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22.8%;
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22.8%;
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21.3%;
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                                                                                        tein; 698 AA.
protein #874
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reductase
                                                                                                                                                                           698 AA.
reductase
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Pred. No.
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Pred. No. 6
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Pred. No. 74;
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Query Match
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RESULT 1045
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Best Local Similarity
RESULT 1044
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Human methionine synthase reductase Cys37Tyr variant.
US2003082676-A1.
01-MAY-2003.
                                  Human Protein 076024,
WO2003016475-A2.
27-FEB-2003.
(GEHO) GEN HOSPITAL
                                                                                                                                                   ABB78282 standard; protein; l
Amino acid sequence of human
WO200263307-A2.
                                                                                                                                                                                                                        Human wm1 protein.
DE19945277-C1.
09-WAR-2000.
(UYMU-) UNIV MUENCHEN MAXIMILIANS LUDWIG.
                                                                                                                                                                                                                                                                                                                                          ADQ39858 standard; protein; 725 AA. Human myocardial infarction-associated W02004058652-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                           ADQ39857 standard; protein; 698 AA.
Human myocardial infarction-associated
WO2004058052-A2.
15-UUL-2004.
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Human wild-type methionine s
US200308676-Al.
01-MAY-2003.
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                                                                               ADD46013 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                (APPL-) APPLERA CORP.
                       (FARB ) BAYER AG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (ROZE/) ROZEN R.
(LECL/) LECLERC D.
(WILS/) WILSON A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (LECL/) LECLERC D.
(WILS/) WILSON A.
(ROSE/) ROSENBLATT D.
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(LECL/) LECLERC D.
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                                                                                                      PHARMACIA & UPJOHN C
h 6.0%;
Similarity 23.8%;
Similarity
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                                                                      076024,
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                                                                      protein; 890 AA.
24, SEQ ID NO 11685.
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22.8%;
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23.8%;
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6.0%;
23.8%;
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k; Score
k; Pred.
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synthase
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In wolframin
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No. 90;
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No. 95;
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No. 90;
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No. 90;
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No.
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No. 1.3e+02;
 71.5; DB 7;
No. 1.3e+02;
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. 1.3e+02;
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           Length 890;
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Query Match
                                                                           08-AUG-2002.

(LIPE-) LIPESPAN BIOSCIENCES INC.

(LIPE-) LIPESPAN BIOSCIENCES INC.

6.0% Score 71.5;

xy Macch

22.4% Pred. No. 6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAB42192 standard;
Human ORFX ORF1956
WO200058473-A2.
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Human MP53 protein
WO2003083047-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABB11404 standard; peptide; Human FLAMINGO 1 homologue, WO200157188-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INCY-) INCYTE GENOMICS INC.
(INCY-) INCYTE GENOMICS INC.
6.0%;
EY Match 1-41arity 22.4%;
                                                                                                                             Human GPCR CELSR2
WO200261087-A2
                                                                                                                                                                                                                                      AAM50866 standard; protein; 2923 AA.
Cadherin EGF LAG seven-pass G-type r
                                                                                                                                                                                                                                                                                                                          AAU07054 standard; protein; 2923 AA.
Human Flamingo protein encoded by cDNA splice variant
                                                                                                                                                                                                                                                                                                                                                                                                           ABUl1556 standard; protein; 2894 AA.
Human MDDT polypeptide SEQ ID 503.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human disease detection and WO2003062379-A2.
                                                    ADC15499 standard;
Human cadherin EGF
                                                                                                                                                   ABP82018 standard;
                                                                                                                                                                                            (STRD ) UNIV STANFORD.
(GENO-) APPLIED GENOMICS INC.
                                                                                                                                                                                                                                                                                            (SMIK ) SMITHKLINE BEECHAM PLC.
                                                                                                                                                                                                                                                                                                                  VO200161003-A1.
                                                                                                                                                                                                                                                                                                                                                                                                      WO200279449-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ML22689 standard; protein;
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BROWN P O.
PEROU C M.
                                                                                                                                                                                                                                                                                                                                                         INCYTE GENOMICS INC.
h 6.0%;
Similarity 22.4%;
                                                                                                                                     ; protein; 2923 AA.
protein SEQ ID NO:524
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             protein;
                                                     protein;
LAG sever
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      protein; 2405 AA.
polypeptide sequence
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22.4%;
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22.4%;
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23.8%;
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SEQ ID NO:1774
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                                                                                                                                                                                                                                                                       71.5; DB 4;
No. 6.6e+02;
                                                                                                                                                                                                                                       receptor
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.5e+02;
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.6e+02;
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.6e+02;
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Query Match
Best Local Similarity
RESULT 1060
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Query Match
Best Local Similarity
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(ROSS/) ROSS D.
(SEIT/) SEITZ R.
(VRIJ/) VAN DE RIJN :
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Human GPCR protein
EP1270724-A2.
                                                                                      AAR31621 standard;
Hepatitis C virus
WO9300365-A2.
                                                                                                                                                                                                                                                                 AAR34468 standard; protein; 3011 
Encoded by full-length Hepatitis 
JP05068562-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                 Human Flamingo polypeptide.
WO200161003-A1.
23-AIG-200
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Human REPTR 9 prote
WO200198354-A2.
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Human GPCR CELSR2,
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Human Protein XP_042739, SE
WO2003016475-A2.
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WO2003016475-A2.
27-FEB-2003.
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(FARB ) BAYER AG.
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Human Protein XP 042739, SEQ ID NO 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (PRIM-) PRIMAL INC.
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h 6.0%; Score
Similarity 23.7%; Pred.
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th 6.0%; Score
Similarity 22.4%; Pred.
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SEQ ID NO
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SEQ ID NO:932.
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22.4%;
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NO:346.
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%; Score 71.5; DB 7;
%; Pred. No. 6.6e+02;
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Q ID NO
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Score
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Pred. No. 6
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No. 6.
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.7e+02;
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.6e+02;
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.6e+02;
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.6e+02;
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.6e+02;
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RESULT 1068

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                                                 Query Match
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G-protein coupled l
US5508384-A.
                                                                                                                                                                                                                      G-protein coupled human interleukin-8 w09405695-A1.
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27-SEP-2001.
(PEKE ) PE CORP NY.
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AAG72377 standard; protein;
Human OR-like polypeptide qu
WO200127158-A2.
                                                                                                                                                                                                                                                                                                      AAG72952 standard; protein;
Human olfactory receptor dat
WO200127158-A2.
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                                                                                    Human olfactory receptor WO200127158-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABB06793 standard;
                                                                                                     WAG72169 standard;
                                                                                                                    (UYNY) UNIV NEW YORK STATE.

CY Match 5.9%;

t Local Similarity 19.7%;
                                                                                                                                                                                                           (UYNY ) UNIV NEW YORK
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                                                         DIGI-) DIGISCENTS.
                                                                                                                                                                                                                                                                                                                                                          (CHIR-) CHIRON SPA.
(GENO-) INST GENOMIC RES.
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                                        Local Similarity
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polypeptide SEQ ID NO 1686.
                                                                                                                                                                peptide; 312 AA.
human interleukin-8
                                                           DEV
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22.9%; P
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19.78;
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22.9%;
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5.9%;
24.5%;
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24.9%;
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29.5%;
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data exploratorium
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polypeptide,
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query
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Best Local Similarity RESULT 1077
        Best Local Similarity
RESULT 1085
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RESULT 1081
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                                     (CHAL) BEHAN D P.
(CHAL) CHALMERS D T.
(LIAW) LIAM C W.
(RUSS) RUSSO J P.
(THOM) THOMSEN W J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        M. catarrhalis protein #1066
US6673910-B1.
                                                                                                                                                                                       ABU19912 standard;
Protein encoded by
                                                                                                                                                                                                                                                                                                                                      ADJ95144 standard;
Novel NOVX protein
WO2003040325-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                    Novel NOVX protein WO2003040325-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABB48413 standard; protein;
Listeria monocytogenes prote
WO200177335-A2.
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                                                                                                Human endogenous
US2003224442-A1.
                                                                                                                                                                     WO200277183-A2.
                                                                                                                                                                                                                                                                   ADP29417 standard; protein; 455 AA.
Human secreted protein SEQ ID #184.
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                                                                                                                    ADI24575 standard; protein; 470 AA.
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                                                                                                                                                          (ELIT-) ELITRA PHARM INC
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PIVE PRIME THERAPEUTICS INC.
5.9%; Score 71;
5.9% Pred. No.
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h 5.9%; Score 71;
Similarity 20.3%; Pred. No.
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                                                                                                         5HT2A serotonin receptor
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sequence
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protein;
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#185.
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(LIPE-) LIPESPAN BIOSCIENCES
5.9%;
ery Match 5.9%;
23.7%;
                                                ADC22747 standard; protein; 471 AA. Human G protein-coupled receptor (G US6555339-B1.
                                                                                                                           ADC22641 standard; protein; 471 AA. Human G protein-coupled receptor (GU8655339-B1.
                                                                                                                                                                                                                    ABP81765 standard; protein; 471 AA.
Human 5-HT2A receptor protein SEQ ID
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Human 5-HT2 receptor sequence.
US6383762-B1.
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TY Match
5.9%; Score 71;
Local Similarity 23.7%; Pred. No.
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(AREN-) ARENA PHARM
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US5661024-A.
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Human serotonin 5-HT2 recept
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20-APR-2000.
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(HERR/) HERRICK-DAVIS
(EGAN/) EGAN C C.
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Human 5-HT2A serotonin receptor.
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(SYNA-) SYNAPTIC
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(LIAW/) LIAW C W.
(BEHA/) BEHAN D P.
(CHAL/) CHALMERS D T
                                                                                                                                                   Human myocardial infarction-
WO2004058052-A2.
                                                                                                                                                                                                                              ADQ39800 standard; protein; Human myocardial infarction. WO2004058052-A2.
                                                                                                                                                                                                                                                                                                                                                                          ADL90125 standard; protein; 471 Human serotonin receptor 5HT2a. US2003167476-Al.
                                                                                  Human myocardial WO2004058052-A2.
                                                                                                      ADQ39798 standard;
                US5885785-A.
                        AAY01626 standard; protein;
Amino acid sequence of the
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US2003170723-A1.
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Query Match
Best Local Similarity 23.5%; Pred. No.
RESULT 1105
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US2002098548-A1.
                                                                                                        Fungal ZBC protein W0200224865-A2
                                 Mouse OCTN3 protein WO200046368-A1.
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(GEHO ) GEN HOSPITAL CORP.
(FARB ) BAYER AG.
                                                                                                                                                                                                                                                                                                                                                                  ADD48660 standard; protein; SRat Protein BAA25372, SEQ ID WO2003016475-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                   (GEHO ) GEN HUDER AG.
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                                                                                                                        ABP35686 standard;
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(GEHO) GEN HOSPITAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABM70440 standard; protein; 493 AA.
Photorhabdus luminescens protein sequence #3537
                                                    AAB20578 standard;
                                                                                      28-MAR-2002.
(MICR-) MICROBIA INC.
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(SYNA-) SYNAPTIC PHARM CORP.
                                                                                                                                                                                                                                          (HINK/) HINKLE G
(SLAT/) SLATER S
(CHEN/) CHEN X.
                                                                                                                                                            ELIT-) ELITRA PHARM
                                                                                                                                                                                                                                GOLD/) GOLDMAN B S.
                                                              Local Similarity
                                                                                                                                   Local Similarity
1109
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                  CHUGAI RES
                                                                                                                                                                                                                                                  ი.
                                          protein;
INST MOLECULAR MEDICINE 5.9%; Score 71; DB 21.4%; Pred. No. 77;
                                                                                                                sequence
                                                                                                                        protein;
                                                                                                                                          M INC.
5.9%;
23.1%;
                                                                    5.9%;
19.1%;
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23.7%;
                                                                                                                                                                                                                5.9%;
26.2%;
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22.0%;
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23.7%;
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22.0%;
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                                                                                                                                                                                                                                                                                               #22014.
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                                            ; 564 AA.
NO:1.
                                                                                                                                                                                                                                                                                                                                                                            545 AA.
D NO 14366.
                                                                                                                  563 AA.
#112.
                                                                                                                                                                                                                                                                                                       546
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    480 AA.
                                                                                                                                                                                                                                                                                                                                                                                                      Score 71;
Pred. No.
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Pred.
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Pred.
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Pred.
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gene
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No.
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76;
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73;
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64;
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77;
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74;
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73;
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62;
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        INC.
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         Length 564;
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                                                                               563;
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Best Local Similarity
RESULT 1119
ID ARR30616 standard; p
DE Polypeptide coded by
PN EP521318-A2.
PD 07-JAN-1993.
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ID ADQ9637
DE T cell
PN WO20040
PD 15-JUL-
PA (ASAH-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity RESULT 1112
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RESULT 1117
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RESULT 1118
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                                                                                                                                                                                                                                               (RAMA/) RAMANATHAN C S
(WEST/) WESTPHAL R.
(FEDE/) FEDER J N.
(LEEL/) LEE L M.
                                                                                                                                                                                ABR62929 standard; protein; 744 AA. Human neurotransmitter transporter. W02003059947-A1.
          AAR30616 standard; protein; Polypeptide coded by Korean EP521318-A2.
                                                                                              ABB60052 standard; protein; Drosophila melanogaster polyWO200171042-A2.
                                                                                                                                                                                                                                                                                                     ADH76500 standard; protein; 727 amino acid human neurot: US2003219774-A1. 27-NOV-2003.
                                                                                                                                                                                                                                                                                                                                                                                                  ABU54636 standard; protein;
Human NOVX polypeptide #95.
WO200281498-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAE21800 standard; protein;
Human HIPHUM 0000029 proteir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO200210210-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABB91532 standard; protein; 676
Herbicidally active polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              T cell activation WO2004058805-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADQ96376 standard;
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                                                                                                                                                                         24-JUL-2003.
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ry Match

t Local Similarity 24.3%;
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ry Match 5.9%;
t Local Similarity 21.3%;
                                                                                                                                                                (FARB )
                                                                                                                                                                                                                                                                                                                                                                               (CURA-) CURAGEN CORP.
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                                                                                                                                       Local Similarity
                                                                                                                                                             BAYER AG.
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                                                                         PE CORP NY
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5.9%; Score
21.3%; Pred. 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      protein;
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24.3%;
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17.7%;
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24.3%;
                                                                                                                                                                                                                            5.9%;
24.3%;
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22.3%;
                                                                                                                                                                                                                                                                                                                           neurotransmitter transporter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein.
                                                                                                         ein; 792 AA.
polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORP.
Core
Core
Core
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          727
                      3010 AA.
HCV full cDNA sequence LBC1
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Pred.
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90;
                                                                                                                                          DB 7;
1.1e+02;
                                                                                                                                                                                                                             DB 8;
1.1e+02;
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1.1e+02;
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99;
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                                                                792;
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Query Match
Best Local S
RESULT 1126
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Best Local S
RESULT 1123
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Best Local Similarity
RESULT 1120
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                                          Best Local Similarity
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                                                                                                                                                                                    WO200277183-A2.
03-OCT-2002.
(ELIT-) ELITRA PHARM INC.
                                                                                                                                                                                                                                    ABU17430 standard; protein; 275 AA. Protein encoded by Prokaryotic essential gene #2957.
                                                                                                                                                                                                                                                                       26-DEC-2002.

26-DEC-2002.

(HELE/) HELENTJARIS T G.

5-9%;

27 Match 5-9%;

21.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAU01287 standard; protein; 218 AA.
Brassica napus fatty acid desaturase, Fad3C, partial sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAR53417 standard; protein;
Blood transmiscible NANBHV p
JP06105690-A.
                                                                                                                                                                                                                                                                                                                                                     ADG47920 standard; protein;
Wheat Arabidopsis-like suga;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Portion of a wheat US6383776-B1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (LUCK-) LUCKY LTD
ABB05467 standard; protein; 291 AA.
Coriolus versicolor aldo/ketoreductase protein SEQ ID NO:2.
                                                                                                                 ABB55033 standard; protein; 285 AA.
Lactococcus lactis protein malG.
                                                                                                                                                                                                                                                                                                                                                                                                                            (HITZ/) HITZ W D. (KINN/) KINNEY A J. (TING/) TINGEY S V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAU97208 standard; protein; 228 AA.
Portion of a wheat sugar transport protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (TYUL-2003.
(UYNE-) UNIV NEWCASTLE VENTURES LTD.
5.9%; Score 70.5; I
FY Match 26.5%; Pred. No. 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABU08333 standard; protein; 228 AA.
Theat sugar transport protein #3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (DUPO ) DU PONT DE NEMOURS & CO E I.

ry Match 5.9%; Score 70.5;
Local Similarity 21.6%; Pred. No. 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (MIAC ) CANADA MIN AGRIC & AGRI-FOOD CANADA.

ry Match
5.9%; Score 70.5; DB 4;
Local Similarity 29.3%; Pred. No. 24;
                                                                                                                                                                                                                                                                                                                                         JS2002199217-A1.
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                                                                                                                                                          Local Similarity
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                                         INRA INST NAT RECH AGRONOMIQUE in 5.9%; Score 70. Similarity 26.1%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ALLEN S M.
                                                                                                                                                                                                                                                                                                                                                                                                5.9%;
21.6%;
                                                                                                                                                             5.9%;
22.8%;
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26.9%;
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26.9%;
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Pred. No.
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Pred.
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Pred. No.
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Pred. No. 25;
                                                                                                                                                             Score 70.5;
Pred. No. 33;
                                                                                                                                                                                                                                                                                                                                                     transport protein
                                                                                                                                                                                                                                                                             % 70.
                                                                                                                                                                                                                                                                       7.5;
25;
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).34;
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7.8e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                218;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
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                                                                                                                                                                                                                                                                                                          Human NOV10a protein. US2004162236-A1. 19-AUG-2004.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADK68232 standard;
Novel NOVX protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADH22355 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (WARI/) WARIISHI H. (KUBI) KUBOTA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      JP2001321171-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO2003085124-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (INCY-) INCYTE CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (CURA-) CURAGEN CORP.
                                                                                                     BENTO P.
BOLLOG F.
BURGESS C.
CASMAN S.
BOKNOR J C.
EDINGER S R.
ELLERMAN K.
FERNANDES B.
GERLACH V.
GROSSE W.
GROSSE W.
GUNTHER B.
GUSSE V.
                                                                                                                                                                                                                                                                                                                                                                                                                 CURAGEN CORP.
                                                                                                                                                                                                                                                                                              ALSOBROOK J.
                                                                                        LEPLEY D.
 ATTURAJAN M.
EYMAN J A.
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Human protein of the invention NOVS5a W02003102155-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28-NOV-2002.
(INSP) INST PASTEUR.
(CNRS) CNRS CENT NAT RECH SCI.
5.9%; Score 70.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human receptor & membrane associated WO2003104395-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Photorhabdus luminescens WO200294867-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (GENO-) GENOME THERAPEUTICS 5.9%; Ty Match 5.9%; t Local Similarity 24.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADA35787 standard; protein; 297 AA.
Acinetobacter baumannii protein #2948
                                                                                                                                                                                                                              ADR49221 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABM70358 standard; protein; 321 AA.
MACDOUGALL J R. MALYANKAR U M.
                                                                                                                                                                                                                                                                                                                                                                                                protein; #79.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                protein; 330 AA.
                                                                                                                                                                                                                                                                                                                                         5.9%;
30.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                             5.9%;
24.2%;
                                                                                                                                                                                                                                                   5.9%;
30.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5.9%;
29.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    protein sequence #3455.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    S CORP.
; Score 70.5; D
; Pred. No. 36;
                                                                                                                                                                                                                                                                                                                                                                                                          343
                                                                                                                                                                                                                                343 AA
                                                                                                                                                                                                                                                    Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                Score
Pred.
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Pred.
                                                                                                                                                                                                                                                                                                                                          Score 70.5;
Pred. No. 44;
                                                                                                                                                                                                                                                    No. 44;
                                                                                                                                                                                                                                                                                                                                                                                                                                70.5;
No. 42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           70.5;
No. 35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    protein
                                                                                                                                                                                                                                                                                                          SEQ
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                                                                                                                                                                                                                                                                Length 343;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 297;
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Query Match
Query Match
Best Local S
RESULT 1141
ID ADS2142
DE Bacter
PN US200
PD 18-D
PA (CA)
PA (H)
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RESULT 1135
ID ADR40543 standard; p
DE Ovine melatonin rece
PN US2004161823-A1.
PD 19-AUG-2004.
PA (PEDE/) FEDER J N.
PA (MINT/) MINTIER G.
PA (RAMA/) RAMANATHAN C
PA (HAWK/) HAWKEN D R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best
RESULT
ID AD
DE Hu
PN US
PD 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         P P P B I
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Best Local
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07-AUG-2003.
(DECO-) DECODE GENETICS EHF.
5.9%;
ery Match
5.9%;
24.2%;
                                                                                                                                                                                                         02-SEP-2004.
02-SEP-2004.
(FARB) BAYER HEALTHCARE AG.
15-98;
17 Match
1 cimilarity 24.28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADI35077 standard; protein; 365 AA. Human prostaglandin E receptor subtype US2003224393-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (PEDE/) FEDER J N. (MINT/) MINTIER G. (RAMA/) RAMANATHAN C S (HAWK/) HAWKEN D R.
                                                                                                                                      ADS21429 standard; protein; 3
Bacterial polypeptide #10462.
US2003233675-A1.
                                                                                                                                                                                                                                                                                                ADR67864 standard; protein; Prostaglandin E2 EP3 III. WO2004074830-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human prostaglandin
US6670134-B1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADL15889 standard; protein; 365 AA.
Human prostaglandin EP3 receptor #3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Prostaglandin-EP3-9
WO9500552-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ovine melatonin receptor O46608 protein. US2004161823-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (RIEG/)
(SHEN/)
(SHIM/)
(SMIT/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAR69518 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                    (ALLR ) ALLERGAN INC.
(UYAR-) UNIV ARIZONA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (DECO-) DECODE GENETICS EHF.
ry Match 5.9%;
t Local Similarity 24.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO2003064471-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human PTGER3 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADR40543 standard; protein;
                                                        (SLAT/) SLATER S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MERI ) MERCK FROSST
                                                                                                                                                                                                   Local Similarity
1141
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1139
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SMITHSON G.
STONE D.
VERNET C.
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SHENOY S.
SHIMKETS I
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                    GOLDMAN
                                                                                                   CAO Y.
                    W
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in isoform, EP3b.
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24.2%;
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23.1%;
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30.0%;
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    v
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Pred.
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Pred.
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Pred.
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Pred.
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Pred. No. 48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 70.5;
Pred. No. 44;
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No. 48;
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No. 48;
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48;
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Length
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Best Local Similarity
RESULT 1142
ID ADF04358 standard, p
DE Bacterial polypeptid
PN U56605709-B1.
PD 12-AUG-2003.
PA (GENO-) GENOME THERA
                                                                               Best Local Similarity RESULT 1150
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RESULT 1146
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RESULT 1145
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAE38520 standard; protein; 374 AA.
Human PTGER3 protein isoform, EP3d.
W02003064471-A2.
07-AUG-2003.
(DECO-) DECODE GENETICS EHF.
DUECY MAtch
5.9%; Score 70
DUECY MAtch
5.9%; Pred. No
                                                                                                                                                                                                                                                                                                                       Prostaglandin-EP3-21 recepto WO9500552-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                         AAW02683 standard;
G-protein coupled
US5508384-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacterial polypeptide #471. US6605709-B1.
           (ALLR )
(UYAR-)
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G-protein coupled
WO9405695-A1.
                                                                                                                  04-DEC-2003
(DECO-) DEC
                                                                                                                                         Human prostaglandin US2003224393-A1.
                                                                                                                                                                                                                                     Human PTGER3 protein WO2003064471-A2.
                                                                                                                                                                                                                                                            AAE38513 standard;
                                                                                                                                                                                                                                                                                 (MERI ) MERCK FROSST CANADA INC.

ry Match 5.9%; Sco
t Local Similarity 24.2%; Pre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADI35075 standard; protein; 374 AA. Human prostaglandin E receptor subtype EP3 US2003224393-A1.
                                                        Human prostaglandin
                                                         ADL15887 standard; protein; 388 AA.
Human prostaglandin EP3 receptor #2
                                                                                                                                                                ADI35061 standard;
                                                                                                                                                                                                                                                                                                                                                                             (UYNY ) UNIV NEW YORK STATE.
ry Match 5.9%;
t Local Similarity 22.9%;
                                                                                                                                                                                                                                                                                                                                                                                                               16-APR-1996.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17-MAR-1994.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (GENO-) GENOME THERAPEUTICS ry Match 5.9%; t Local Similarity 33.3%;
                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
            UNIV ARIZONA.
                                                                                          DECODE GENETICS EHF. h 5.9%; Similarity 24.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        UNIV NEW YORK STATE.
h
5.9%;
Similarity 22.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DECODE GENETICS EHF.
h 5.9%;
Similarity 24.2%;
                        ALLERGAN INC.
                                                                                                                                                                                     E GENETICS EHF.
5.9%;
arity 24.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                        ; peptide; 379 rat serotonin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein; 379 rat serotonin
                                                                                                                                                    protein; 388 AA.
1 E receptor subtype EP3
                                                                                                                                                                                                                                               protein; 388 AA.
ln isoform, EP3c.
                                                                                                                                                                                                                                                                                                                                            receptor
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  ហ
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2 receptor.
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                                                                                                                                                    protein
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Best Local Similarity
RESULT 1155
ID ADI35067 standard; p
DE Human prostaglandin
PN US2003224393-A1.
PD 04-DEC-2003.
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RESULT 1151
ID ADS::--
RESULT
ID AD
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Best Local Similarity
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Human prostaglandin E receptor subtype EP3
US2003224393-A1.
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                                                                                                                                                                                                                            ADL15898 standard; protein; 390 AA.
Human prostaglandin EP3 receptor #4.
US6670134-B1.
                                                                                                                                                                                                                                                                                                                   Human prostaglandin
US2003224393-A1.
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WO9500552-A1.
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                              ADR70434 standard; protein;
Human prostaglandin E2 EP3 ;
                                                                                                                                                                                                                                                                                                                                            ADI35069 standard; protein; 390 AA.
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ry Match 5.9%;
t Local Similarity 24.2%;
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                    Human prostaglandin
WO2004074842-A2.
                                                                                                                                 ADL15885 standard; protein; 390 AA.
Human prostaglandin EP3 receptor #1.
                                                                                                                                                                                       (MILR ) ALLERGAN INC. (UYAR-) UNIV ARIZONA.
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ry Match 5.9%;
c Local Similarity 24.2%;
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cy Match 5.9%;
Local Similarity 24.2%;
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                                                                                      (ALLR ) ALLERGAN INC.
(UYAR-) UNIV ARIZONA.
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Local Similarity 24.2%;
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BAYER HEALTHCARE AG
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in isoform, EP3a2.
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in isoform, EP3al
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n E2 EP3 II polypeptide
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24.2%;
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Pred. No. 53;
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Best Local
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                                                                  Query Match
Best Local Similarity
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Human EP3-V receptor.
JP10113185-A.
06-MAY-1998.
                                                                                                        Human prostaglandin WO200261087-A2.
                                                                                                                  ABP81904 standard; protein; 402
Human prostaglandin E2 receptor
                                                                                                                                                                                                                                                                 ADI35073 standard; protein; 393 AA.
Human prostaglandin E receptor subtype
US2003224393-A1.
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S:ry Match 5.9%;
It Local Similarity 24.2%;
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                                                AAE38522 standard;
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Human prostaglandin E receptor s
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Human PTGER3 protein isoform, EP3-VI.
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Human PTGER3 protein isoform, EP3e.
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                                                                                      (LIFE-) LIFESPAN BIOSCIENCES
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h 5.9%;
Similarity 24.2%;
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                                      protein; 402 AA.
in isoform, EP3-V
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subtype
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RESULT 1173
ID ADI3506
DE Human p
PN US20032
PD 04-DEC-
PA (DECO-)
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RESULT
ID AD
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PD 04
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**PGER3 protein isoform,
07-AUG-2003
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US2003224393-A1.
                                                                                                                                                                                                                                   WO2003064471-A2.
07-AUG-2003.
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Protein #69 with in
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US2003224393-A1.
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                                     Human prostaglandin
US2003224393-A1
                                                                                                                        AAE38515 standard;
                                                                                                                                                                                          ADI35071 standard;
                                                                                                                                                                                                                                                   AAE38518 standard; protein; 425 AA.
Human PTGER3 protein isoform, EP3f.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADO29620 standard;
                                                      DI35065 standard;
                                                                                                        WO2003064471-A2.
                                                                                                                                                                                                           (DECO-) DECODE GENETICS EHF.
ry Match 5.9%;
t Local Similarity 24.2%;
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(VAND-) VAN ANDEL INST.
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            DECODE GENETICS
5.
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protein isoform, EP3h.
                                                                      GENETICS EHF.
5.9%;
rrity 24.2%;
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SEQ ID NO:722.
                                            protein; 433 AA.
1 E receptor subt
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n E receptor subtype
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m, EP3g.
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No. 59;
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Query Matc
Best Local
RESULT 1184
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Best Local Similarity
RBSULT 1183
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ID AAW98431 standard;
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RESULT 1185
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                                                                        Protein encoded I WO200277183-A2. 03-OCT-2002.
                                                                                                                                                                                                                         (ALLE/) ALLEN S M.
(HITZ/) HITZ W D.
(KINN/) KINNEY A J.
(TING/) TINGEY S V.
                                                                                                                                                                                                                                                                                                                                            Wheat sugar transport protein encoded US6383776-B1. 07-MAY-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Staphylococcus epidermidis ORF amino US6380370-B1.
Bacterial polypeptide #5442.
US2003233675-A1.
                                                                                                                                                      ADG47930 standard; protein; Wheat Beta-vulgaris-like sug US2002199217-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                            Protein encoded WO200277183-A2. 03-OCT-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Staphylococcus epidermis polypeptide US2004147734-A1.
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WO9843478-A1.
                                                                                            ABU27418 standard;
Protein encoded by
                                                                                                                                                                                                                                                                          Wheat sugar tran
US2002178468-A1.
                                                                                                                                                                                                                                                                                              ABU08338 standard;
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Protein encoded by
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          08-OCT-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADS06092 standard; protein;
                                                                                                                                             (HELE/) HELENTJARIS
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ry Match 5.9%; Score
t Local Similarity 20.5%; Pred
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5.9%;
h
Similarity 23.7%;
                                                               ELITRA PHARM
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                                                                                                                                                                                                                                                                                     transport
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ort protein
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Prokaryotic (
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5.9%;
26.0%;
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Prokaryotic essential
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23.1%;
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24.0%;
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26.0%;
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20.5%;
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26.0%;
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sugar trans
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in #4.
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                         556 AA
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Pred. No. 70;
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No.
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83;
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RESULT 1188
ID ABW0268
DE Rattus
PN US20031
PD 31-JUL
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                                                                                                                         RESULT 1193
                         AAG39555 standard; protein; Arabidopsis thaliana protein EP1033405-A2.
                                                                                               ADG47941 standard; protein; 740 Arabidopsis thaliana-like sugar US2002199217-A1.
                                                                                                                                                                       Human prostate cancer antigen W0200055174-A1.
                                                                                                                                                                                                                                                                                                                                                                                               AAM78767 standard;
Human protein SEQ
WO200157190-A2.
                                                                                                                                                                                                                                                                                                                                  ADJ64315 standard; protein; 662 AA. Cartilage differentiation inhibiting
                                                                                                                                                                                                                                                                                                                                                                             09-AUG-2001.
(HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                           ABB92892 standard; protein; 700 Herbicidally active polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADD46023 standard; protein; Rat Protein P23978, SEQ ID W02003016475-A2.
                                                                                                                                                                                                                                          07-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rattus norvegicus
US2003143729-A1.
                                                                                                                                                  (HUMA-) HUMAN GENOME SCI INC. (ROSE/) ROSEN C A.
                                                                                                                                                                                                                                                    #0200210210-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABW02687 standard;
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(GEHO ) GEN HOSPITAL
(FARB ) BAYER AG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (HINK/) HINKLE G
(SLAT/) SLATER S
(CHEN/) CHEN X.
                                                                              (HELE/) HELENTJARIS
                                                                                                                                                                                                                                                                                                                   .2-FEB-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                  (SYNA-) SYNAPTIC PHARM CORP.

CY Match 5.9%;

Local Similarity 20.1%;
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1187
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Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; protein; 599 AA.
neuronal GABA transporter (GAT-1)
                                                                                                                                                                                                                                                                                                                                                                                                         in NO 1429.
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5.9%;
22.7%;
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5.9%;
22.8%;
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19.5%;
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22.4%;
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21.1%;
5.9%;
21.3%;
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25.8%;
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20.1%;
                                   protein
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NO 11695.
                                  ; 766 AA.
In fragment
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transport
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SEQ
70.5; DB 3;
No. 1.3e+02;
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86;
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96;
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.2e+02;
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Best Local
RESULT 1204
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RESULT 1199
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RESULT 1202
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                                                                    Human gravin
US6090929-A.
                                                                            AAB15380 standard; protein; 1780 Human gravin protein sequence.
                                                                                                        (UYOR-) UNIV OREGON HEALTH SCI.

STY Match 5.9%; Score
St Local Similarity 34.8%; Pred.
                                                                                                                                              AAW53863 standard; peptide;
Human gravin polypeptide.
US5741890-A.
                                                                                                                                                                                                                            ADM29274 standard; protein; Human novel protein NOV2b. WO2003064628-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 (CHEM-) CHEMGENICS PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Candida albicans chitin synthase W09716540-A1.
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                                     18-JUL-2000.
(UYOR-) UNIV OREGON HEALTH SCI.
5.9%; Score
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                                                                                                                                                                                                                                                                                                                     Human NOVX protein
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WO2003093444-A2.
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ry Match 5.9%;
t Local Similarity 22.3%;
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          AAO17365 standard;
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          protein; 1781 AA
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k ion channel
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                            DB 3;
.3e+02;
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.4e+02;
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.4e+02;
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.4e+02;
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.5e+02;
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RESULT 1213
ID ABB697
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PD 7
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RESULT 1212
ID AAG34240 standard; F
DE Arabidopsis thaliana
PN EP1033405-A2.
PD 06-SEP-2000.
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                                                                                    AAG34240 standard; protein; 235 AA. Arabidopsis thaliana protein fragment EP1033405-A2.
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Arabidopsis thaliana
EP1033405-A2.
                                 ABB69790 standard; prote
Drosophila melanogaster
                                                                                                                                                        Alloiococcus otitis WO2003048304-A2.
                                                                                                                                                                                                                                                                                                                                              Arabidopsis thaliana EP1033405-A2.
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7.9%;
ry Match
t Local Similarity 21.6%;
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Angiogenesis-associated hum
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ry Match 5.9%; (
Local Similarity 34.8%; )
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antigenic protein
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polypeptide
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in fragment
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NO: 716.
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4.3e+02;
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Best Local Similarity
RESULT 1214
ID ADS96502 standard; p
DE Drosophila melanogas
PN W0200403999-A2.
PD 13-MAY-2004
PA (SYGN) SYNGENTA PAR
Best RESULT 1
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ID ADK4848
DE Strepto
PN US66997
PD 02-MAR-
PA (GENO-)
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RESULT
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RESULT 1216
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RESULT 1215
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                                                                                                                      Human G protein-coupled receptor w0200022129-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                  AAG53761 standard; protein; Arabidopsis thaliana proteir EP1033405-A2.
                                                              AAY90647 standard; protein;
Human mutant G protein-coupl
                                                                                                                                                                                    11-MAY-1995.
(ALCO-) ALCOHOLISM &
                                                                                                                                                                                                     AAR72985 standard; protein;
Epsilon opioid receptor.
WO9512670-A1.
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(GENO-) GEN
                                                                                                                                                                                                                                                                            Streptococcus
US6699703-B1.
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Protein encoded by
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EP1033405-A2.
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Arabidopsis thaliana protein fragme
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WO2004078949-A2.
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Haemophilus influenzae (NTHi) protein
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03-OCT-2002.
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h 5.9%; Score
Similarity 18.3%; Pred.
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protein,
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27-DEC-2001.
(TAKE) TAKEDA CHEM IND LTD.
Match 5.9%; $
5.9%; $
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                                     ABP81897 standard; protein; 333 A Human G protein-coupled receptor WO200261087-A2.
                                                                                                                ABJ37874 standard; p
GPR7 ligand related
WO2002102847-A1.
                                                                                                                                                                                                                                                                       ABG65918 standard;
G protein-coupled r
WO200244368-A1.
                                                                                                                                                                                           ABU61448 standard;
Screening method re
WO200293161-A1.
                                                                                                                                                                                                                                                                                                                                                              ABB84723 standard; protein; 333 AA.
Human GPR8-ligand related protein #
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Human G-protein receptor 8, GPR
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WO200127632-A2.
                                                                                                                                                                        21-NOV-2002.
(TAKE ) TAKEDA CHEM
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ry Match 5.9%;
t Local Similarity 23.6%;
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Human GPR8-ligand
                                                                                                                                                                                                                                                                06-JUN-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (WILL/) WILLIAMS
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Human G-protein receptor 8,
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th 5.9%;
Similarity 23.6%;
 LIPESPAN BIOSCIENCES h 5.9%; similarity 23.6%;
                                                                                              TAKEDA CHEM
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                                                                                                                                                                                                    1; protein; 333 AA. related protein #1.
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                                                                                                                                                                                                                                                                                protein; 333 AA. receptor related
                                                                                                                        protein; 333 AA
1 human protein 8
                                                                          I IND LTD.
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RESULT 1235
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                                    Best Local Similarity SULT 1240
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(LIAW/) LIAW C W.
(BEHA/) BEHAN D P.
(CHAL/) CHALMERS D
                                                              (LIAW/) LIAW C W.
(BEHA/) BEHAN D P.
(CHAL/) CHALMERS I
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ADG12852 standard; protein; Human wild-type hGPR8 amino WO2003097795-A2.
                                                                                                                                                                                                                                                                       ADG41976 standard; protein; Human GPR8 polypeptide. JP2003009867-A.
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Human G protein-coupled rece
US6555339-B1.
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                                                                                                 Mutated human GPR8
US2003105292-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                 ADC51793 standard;
Human GPR8, SEQ ID
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US2003105292-A1.
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WO2003057236-A1.
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ry Match 5.9%;
t Local Similarity 23.6%;
                                                                                                                      ADH14164 standard;
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SEQ ID NO:84.
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Best Local Similarity
RESULT 1248
ID AD028778 standard; p:
DE Human GPR8-enhanced:
PN US2004091946-Al.
PD 13-MAY-2004.
PA (OAKL/) OAKLEY R H.
PA (LAPO) LAPORTE S A.
PA (LAPO) CARON M G.
PA (CARO/) CARON M G.
RESULT 1249
ID ADG1285
DE HA tagg
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RESULT 1243
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                                         (OAKL/) OAKLEY R H.
(BARA/) BARAK L S.
(LAPO/) LAPORTE S A.
(CARO/) CARON M G.
                                                                                                                                                                                                                                                                                                  Human HA tagged wild-type hgpr8 W02003097795-A2.
                                                                                                                                                                Human hGPR8-enhanced receptor
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Human GPCR GPR8, SEQ ID NO:802.
                                                                                                                                                                                                                                   Human calcium channel WO200252003-A2.
                                                                                                                                                                                                                                                                                                                                                                              Human GPR8 ligand WO2004080485-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADQ19919 standard;
Human soft tissue
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                                                                                                                                                                                                                                                   ABG30839 standard;
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HA tagged
          ADG12858 standard;
                                                                                                 Human GPR8-enhanced
                                                                                                          ADO28778 standard; protein; 364 AA
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hGPR8-enhanced rec
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protein SeqID
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SEQ ID NO:73.
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receptor amino
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in; 378 AA.
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Best Local Similarity
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RESULT 1252
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RESULT 1251
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RESULT 1256
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Mouse GPCR OXTR, SEC
WO2004040000-A2.
13-MAY-2004.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (RAMA/) RAMANATHAN C
(GOPA/) GOPAL S.
(MINT/) MINTIER G A.
(FEDE/) FEDER J.
AAB16787 standard; protein; 475 AA. Human transporter and ion channel-24 W0200192304-A2.
                                                                                                                                                                          אינאיא standard; protein; 470 Acinetobacter baumannii protein מומגקבים ביי
                                                                                                                                                                                                                                                                                                                                 ABG99947 standard; protein;
Human novel polypeptide #60
WO200274961-A1.
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                                                                                         Photorhabdus luminescens protein WO200294867-A2.
                                                                                                             ABM67264 standard; protein; 474 AA.
                                                                                                                                                                                                                                                   E. faecium protein
US6583275-B1.
                                                                                                                                                                                                                                                                        ADC96947 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                          Human protein,
EP1293569-A2.
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                                                           (INSP ) INST PASTEUR.
(CNRS ) CNRS CENT NAT RECH SCI.
                                                                                                                                                                                                             (GENO-) GENOME THERAPEUTICS
ry Match 5.9%;
t Local Similarity 25.9%;
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(REAS-) RES ASSOC
                                                                                                                                                                                                                                                                                                                                                                                                                                   ADA54410 standard;
Human protein, SEQ
                                                                                                                               Local Similarity
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h 5.9%;
                                                                                                                                                                                                                                                                                                               HYSEQ INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               seQ ID NO:693.
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BIOTECHNOLOGY.
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ID 1978.
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22.9%;
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            (TRICH-24)
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Query Match

INCYTE GENOMICS
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Query Match
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RESULT 1259
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                                                                                                                                            Query Match
                                                                                           Human diagnostic and therapeutic pprotein MO2004033973-A2.
                                                                                                                                                                Group B Streptococcus protein; 640 AA. WO200006736-A2.
                                                                                                                                                                                                                                                                                                                 ABU18262 standard;
Protein encoded by
WO200277183-A2.
                                                                                                                                                                                                                                                     ABU33453 standard;
Protein encoded by
                                                                                                                                                                                                                                                                                                                                                                                         Human polypeptide
WO200153312-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human TRICH-20 protein.
WO200212340-A2.
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                                  ADL04660 standard; protein;
M. catarrhalis protein #426.
                                                                                                                                                                                                                          03-OCT-2002.
(ELIT-) ELITRA PHARM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABM72414 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAE21176 standard;
                                                                              (INCY-) INCYTE CORP.
                                                                                                                                                    (MICR-) MICROBIAL TECHNICS LTD.
                                                                                                                                                                                                                                              VO200277183-A2.
                                                                                                                                                                                                                                                                                                 (ELIT-) ELITRA PHARM
                                                                                                                                                                                                                                                                                                                                                                                                          AM39017 standard;
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INCY-) INCYTE GENOMICS INC.
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THERAPEUTICS 5.9%;
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Prokaryotic e
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Prokaryotic esse
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protein #1654.
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767;
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Best Local Similarity
RESULT 1267
ID AAR53921 standard; pi
DE HCV fusion protein cc
PN JP06092996-A.
PD 05-APR-1994.
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RESULT
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RESULT 1275
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RESULT 1269
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                                                                                                                                                                                                                            Human G protein-coupled receptor (G WO200168858-A2.
                                                                                                                                                                                                                                                                                                               Alloiococcus otitis antigenic pr
W02003048304-A2.
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                            '(MÎAC') CANADA MIN AGRIC & AGRI-FOOD CANADA.

"YMAtch 5.8%; Score 69.5; DB

"L Local Similarity 29.3%; Pred. No. 31;
                                                                               AAU01288 standard; protein; 218 AA. Brassica napus fatty acid desaturase,
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13-MAY-2003.
                                                                                                                                                     Novel G protein US2002058306-Al.
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ry Match 5.8%;
t Local Similarity 26.0%;
                                                                                                                                                                         ABG60737 standard;
                                                                                                                                                                                                                           20-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                             ADA33664 standard; protein; 198 AA.
Acinetobacter baumannii protein #825
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         ADB09278 standard; protein;
                                                                       ₩O200125453-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                (HUMA-) HUMAN GENOME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (HINK/) HINKLE G J. (SLAT/) SLATER S C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (SHIM/) SHIMOTOYA K.
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                                                                                                                                                                                                                                                                                                                                                            Local Similarity
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3%; Score 69.5; D
9%; Pred. No. 29;
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; Score 69.5; I
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id 286.
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         247 AA.
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to N-terminal of ORF
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                                                                                partial sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human olfactory receptor polypeptide, WO200127158-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Streptomyces hygroscopicus ABC transporter. W02003082909-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22-APR-2003.

(GENO-) GENOME THERAPEUTICS CORP.

127 Match
15.8%; Score 69.5; I

127 Armilarity 22.1%; Pred. No. 42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABG66935 standard; protein; 253 AA.
Novel G-protein coupled receptor related
W0200240539-A2.
AAU95729 standard; protein; 308 AA. Human olfactory and pheromone G proWO200224726-A2.
                                                                                                                                                               ABP95703 standard; protein; 308 AA. Human GPCR polypeptide SEQ ID NO 216. WO200216548-A2.
                                                                                                                                                                                                                                                                                                                                    Human olfactory WO200168805-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABB44525 standard; protein; 308 AA. Human GPCR3 polypeptide SEQ ID NO 9 WO200174904-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pseudomonas aeruginosa polypeptide US6551795-B1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABB62542 standard; protein; 261 AA. Drosophila melanogaster polypeptide WO200171042-A2.
                                                                                                                                                                                                                                                                                                                                                        AAU24742 standard; protein; 308 AA.
Human olfactory receptor AOLFR242.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              11-OCT-2001.
(CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12-JUN-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19-APR-2001.
(DIGI-) DIGISCENTS.
(YEDA) YEDA RES &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23-MAY-2002.
(CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
1281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PE CORP NY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WYETH HOLDINGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        $ DEV CO LTD.
5.8%; S.
7 20.9%; P
                                                                                                                          TECHNOLOGY CORP
                                                                                5.8%;
20.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5.8%;
24.2%;
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5.8%;
26.0%;
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20.9%;
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20.9%;
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21.0%;
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27.7%;
                                                                                Score 69.
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Pred. No.
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Pred.
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Pred.
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Pred.
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Pred.
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Pred.
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Pred.
                     protein-coupled
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          No 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           69.5; I
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69
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                                                                   3.5;
50;
                                                                                                                                                                                                                                         9.5;
50;
                                                                                                                                                                                                                                                                                                                                                                                                            9.5;
50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       y.5;
40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4.5;
50;
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38;
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. 47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        명
                                                                                                                                                                                                                                                                         DB 4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              B
                                                                                                    DB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           <u>ب</u>
                     receptor
                                                                                                                                                                                                                                                                       Length
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                                                                                                  Length
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Query Match
Best Local S:
RESULT 1291
ID ADE37749 |
DE Yeast ARV
PN US2003186|
PD 02-OCT-20
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                                                                                                                                                                                                                                                                                                        Best Local Similarity RESULT 1288
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                                                                                                                                                                                                                   Best Loca
RESULT 1289
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RESULT 1290
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                                         Yeast An.
US6566512-B1.
20-MAY-2003.
1 (UYCO) UNIV COLUMBIA NEW YORK.
5.8%; Scot
                                                                                                                                                     Query
                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
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(NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
(ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.
(ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.
5.8%; Score 69.5; DB 7;
ery Match
5.0%; Pred. No. 50;
ADE37749 standard; protein; 321 AA.
Yeast ARV1 (ARE-2 Required for viability).
US2003186879-A1.
02-OCT-2003.
                                                                                                                                                                                                                                                            ABR01671 standard; protein; 316 AA. Human G protein coupled receptor SEQ WO2003000735-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAU85362 standard; protein; G-coupled olfactory receptor WOZ00198526-A2.
                                                                                                          ADC33485 standard;
Yeast ARV1.
                                                                                                                                                                          03-JUN-1999
                                                                                                                                                                                    Chlamydia pneumoniae WO9927105-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human GPCR3 prot
US2003195335-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human GPCR protein EP1270724-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28-MAR-2002
                                                                                                                                                                                              AAY35360 standard; protein; 321 AA.
Chlamydia pneumoniae involved in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABW02126 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADC86333 standard;
                                                                                                                                                                                                                             (DECO-) DECODE GENETICS EHF.
TY Match 5.8%;
t Local Similarity 20.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (SENO-) SENOMYX INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (CHEM-) CHEMCOM SA.
                                                                                                                                                                                                                                                                                                                                                               STON/)
                                                                                                                                          ocal Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ocal Similarity
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SZEKERES E S.
CASMAN S.
ALSOBROOK J P.
BURGESS C E.
                                                                                                                                                                                                                                                                                                                                                            SHENOY S.
KEKUDA R.
GANGOLLI E A.
STONE D J.
                                                                                                                                                                                                                                                                                                                                       SMITHSON G.
MACDOUGALL J
                                                                                                                                                                                                                                                                                                                                                                                                                 PADIGARU M.
TAYLOR S.
TCHERNEV V T.
SPYTEK K A.
                                                                                                                                                                GENSET.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    protein; 308 AA.
SEQ ID NO:786.
                                                                                                                    protein;
                                                                                                                                                                                                                                                                                                                   5.8%;
20.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5.8%;
20.9%;
                                                                                                                                          5.8%;
21.4%;
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20.9%;
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or #223.
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                                                                                                                     321
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Pred.
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Pred.
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Pred.
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Pred.
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Pred. No. 50;
                                                                                                                     Ā
                                                     No. 53;
                                                                                                                                          No. 53;
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                                                                                                                                                                                                                                                                                                                   No. 50;
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                                                                                                                                                                                                virulence
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                                                                Length
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                                                                                                                                                                                                                                          Length 316;
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                                                                                                                                                      321;
                                                                                                                                                                                                                                                                                                                                308;
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Best
RESULT 1
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RESULT 1294
ID ADH10684 standard; p
DE Rat Sprague-Dawley p
PN W02003104484-A1.
PD 18-DEC-2003.
PA (META-) METABOLEX IN
                                                                                                                                                                                       Query Match
Best Local S
RESULT 1298
ID ABB47613
DE Listeria
RESULT ID ADI
                                                                                                                                                                                                                                                                                          Query Match
Best Local S
RESULT 1297
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Best L
RESULT 1
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Best Local Similarity
RESULT 1292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity RESULT 1293
                                                                                                                               RESULT
                                                         Query Match
Best Local S
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                                                                                                                                                                                                                                                                                                                                      LPA receptor-related amino acid sequence W0200112838-A2.
                                                                                                                                                                                                                                                             ABG76099 standard; protein;
Human lysophosphatidic acid
US6485922-B1.
                                                                                                                                                                                                                                                                                                                                                                          409919513---.
22-APR-1999.
(LXRB-) LXR BIOTECHNOLOGY INC.
5.8%; Score 69.5; [
50.2%; Pred. No. 67;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (UYCO ) UNIV COLUMBIA NEW YORK.
                                                                                                Protein encoded WO200277183-A2.
                                                                                                          ABU32698 standard;
Protein encoded by
                                                                                                                                                                               Listeria monocytogenes WO200177335-A2.
                                                                                                                                                                                       ABB47613 standard; protein; 400 AA.
Listeria monocytogenes protein #317
                                                                                                                                                                                                                                                                                                                                                                                                                           Human EDG-2 p
WO9919513-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rat Sprague-Dawley putative WO2003104484-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Propionibacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Propionibacterium acnes immunogenic protein #14035
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAU53139 standard;
                                                                           03-OCT-2002.
(ELIT-) ELITRA PHARM
                                                                                                                                                                                                                                       (ATAI-) ATAIRGIN TECHNOLOGIES INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                             AAY05489 standard; protein; 382 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO2003033515-A1.
24-APR-2003.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200181581-A2.
                                      ADL12060 standard;
                                                                                                                                                                                                                                                                                                     (ATAI-) ATAIRGIN TECHNOLOGIES INC.
ry Match 5.8%; Score
t Local Similarity 20.2%; Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADH10684 standard; protein;
                   WO2003002137-A2
                                                                                                                                                           (INSP ) INST PASTEUR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (META-) METABOLEX INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NBM49658 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (CORI-) CORIXA CORP
                                                                                                                                    Local Similarity
                                                                                                                                                                                                                    Local Similarity
                                                          Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                cal Similarity
DEVELOGEN ENTWICKLUNGSBIOLOGISCHE FORSCH.
                                                                                                                                                                                                                                                                                                                                                                                                                                   protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   acnes
                                                                                                          protein; 400
Prokaryotic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           protein; 327 AA.
                                     protein;
                                                         5.8%;
22.9%;
                                                                              INC.
                                                                                                                                      5.8%;
22.9%;
                                                                                                                                                                                                                      5.8%;
20.2%;
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22.0%;
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25.5%;
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25.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   predicted
                                                                                                                                                                                                                                                                       382 AA.
(LPA) receptor
                                                                                                                    400 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             327 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  354 AA.
GCR polypeptide
                                     401 AA
                                                         Score 69.
Pred. No.
                                                                                                                                       Score
Pred.
                                                                                                                                                                                                                      Score 69.
Pred. No.
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Pred.
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Pred.
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Pred.
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                                                                                                                                                                                                                                                                                                     Pred.
                                                                                                           essential
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                                                                                                                                      No.
                                                                                                                                                                                                                                                                                                       No
69
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8 6
8
                                                    7.5;
72;
                                                                                                                                                                                                                  y.5;
67;
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61;
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                                                                                  Novel S. pneumoniae
US6800744-B1.
05-OCT-2004.
(GENO-) GENOME THERA
                                                                                                                                                                  Streptococcus pneumoniae US6699703-B1.
                                                                                                                                                                                                                                        Arabidopsis thallana protein (EP1033405-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Drosophila melanogaster polypeptide W0200171042-A2.
                                   AAG30874 standard; protein; 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABB66992 standard; protein; 428 AA. Drosophila melanogaster polypeptide
                                                                                                                                        (GENO-) GENOME THERAPEUTICS ry Match 5.8%; Local Similarity 24.4%;
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                                                                                                                      ADR95087 standard; protein;
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5.8%; Score 69.5;
Similarity 20.9%; Pred. No. 79;
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DEVELOGEN ENTWICKLUNGSBIOLOGISCHE
1. 5.8%; Score 69.5;
Similarity 20.9%; Pred. No. 75;
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                     04-MAY-2000.

04-MAY-2000.

(CONN-) CONNAUGHT LAB LTD.

5.8%;

TO Match 5.8%;

21.4%;
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(HINK/) HINKLE G J.
(SLAT/) SLATER S C.
(CHEN/) CHEN X.
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                                                             WO200024765-A2.
                                                                                                                                  ADR13717 standard;
Amidase, SEQ ID 54.
WO2004069848-A2.
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WO200024765-A2.
                                                                                                                                                                                                                                                            EP1033405-A2.
                                                                                                                                                                                                                                                                                                                                         AAY41278 standard; protein; 500 AA. Fusion protein containing rabbit prostaglandin w09953033-A1.
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Klebsiella pneumoniae polypeptide s
msccinosc-si
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Bacterial polypeptide #17545
US2003233675-A1.
ABU26764 standard;
Protein encoded by
                                                                              AAY92828 standard; protein;
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                                                                                                                                                                                                                                                                                      AAG30873 standard; protein;
                                                                                                                                                                                                04-MAY-2000
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(UYVA-) UNIV VANDERBILT.
                                                                                                                 19-AUG-2004.
(DIVE-) DIVERSA CORP.
                                                                                                                                                                                      (CONN-) CONNAUGHT LAB
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(SLAT/) SLATER S
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CPN100557 antigen.
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                                                                             ADE09321 standard; protein; Novel protein-related contig WO2003054152-A2.
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Human SLC22A related proteir
W0200299053-A2.
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18-MAR-1999.

(CHUG-) CHUGAI RES INST MOLECULAR MEDICINE INC.
5.8%; Score 69.5; DB 2;
2ry Match
5.8%; Srore 69.5; DB 2;
2ry Match
26.3%; Pred. No. 1.1e+02;
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03-OCT-2002.
(ELIT-) ELITRA PHARM
                                                                                                                                                                               ABO07242 standard; protein;
Human p53 modifying protein,
WO200299122-A1.
                                                                                                                                                                                                                                                                                                                                                                           ABB82979 standard; protein; 557 AA.
Human SLC22A related protein-GenBank
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Human carnitine transporter
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Novel protein-related WO2003054152-A2.
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                       ADE09261 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                     (HYSE-) HYSEQ INC.
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Prokaryotic (
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e 69.5; DB 3;
. No. 1.1e+02;
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No. 1.1e+02;
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No. 1.1e+02;
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.1e+02;
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                                                                                                                                      DB 6;
.1e+02;
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.1e+02;
                                              DB 7;
.1e+02;
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RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13-MAX-2003.
13-MAX-2003.
(GENO-) GENOME THERAPEUTICS CORP.
12Y Match
1---1 similarity 20.2%; Pred
                                                                                                                                                                  ABU32703 standard;
Protein encoded by
WO200277183-A2.
                                                                                                                                                                                                                                               Listeria monocytogenes protein #114 W0200177335-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                     ABB89665 standard;
Human polypeptide
WO200190304-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADP23817 standard; protein; 55 PRO polypeptide SEQ ID NO:995.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (HYSE-) HYSEQ INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABO62908 standard; protein; 564 AA.
Klebsiella pneumoniae polypeptide s
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADA34637 standard; protein; 559 AA.
Acinetobacter baumannii protein #1798.
                                                                                           ABP65234 standard; protein; 599 AA.
Hypoxia-regulated protein #108.
                  AAE38584 standard;
                                                                                                                                                                                                                                                                                                                                                                                                              29-NOV-2001.
(HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (GENO-) GENOME THERAPEUTICS CORP.

Y Match 5.8%; Score 69.
Local Similarity 23.6%; Pred. No.
                                       (OXFO-) OXFORD BIOMEDICA UK LTD.

CY Match 5.8%; Sco
Local Similarity 19.6%; Pre
                                                                                                                                                                                                                                                                                                                (REAS-) RES ASSOC BIOTECHNOLOGY.
                                                                                  10200246465-A2.
                                                                                                                                               ELIT-) ELITRA PHARM INC.
                                                                                                                                                                                                                                                                                     Local Similarity
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         d; protein;
transporter
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                                                                                                                                                                             protein; 579
Prokaryotic e
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21.1%;
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22.7%;
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22.4%;
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21.1%;
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26.3%;
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26.3%;
        protein.
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                                        Score 69.5
Pred. No.
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Pred. No.
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Pred.
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Pred.
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Pred. No.
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.2e+02;
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.2e+02;
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Query Match Best Local Similarity
RESULT 1337
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RESULT 1343
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                                                                                                     Best Local Similarity RESULT 1344
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                                                                                                                                                                                                                                                                                                                    Human vesicle membrane protein-like WO9921994-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAY41285 standard; protein; 656 AA.
CI-77A-TL fusion protein encoded by
W09953033-A1.
21-OCT-1999.
ADO09827 standard; protein; 681 AA.
Hamster SGLT homologue protein SEQ ID NO:50.
                                                                                 ADQ96536 standard; protein; cell activation associated
                                                                                                                                                                 ADJ64317 standard; protein; 663 AA. Cartilage differentiation inhibiting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Staphylococcus
US6380370-B1.
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(FARB ) BAYER AG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO2003016475-A2.
27-FEB-2003.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADD46025 standard; protein; 599 AA.
Human Protein P30531, SEQ ID NO 11697.
                                                                                                                                   (ASAH ) ASAHI KASEI
                                                                                                                                                                                                                                         US2003175787-A1.
                                                                                                                                                                                                                                                                                                       (INCY-)
                                                                                                                                                                                                                                                                                                                                                                                       (BUSH/) BUSH D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABP40194 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (MILL-) MILLENNIUM PHARM INC.
                                                                                                                                                                                                                                                    Human vesicle membrane
                                                                                                                                                                                                                                                              ADM83092 standard;
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                                                                                                                                                                                                                                                                                                      INCYTE PHARM INC.
                                                                                                                                                                                                                    INCYTE CORP
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epidermidis (
                             I PHARMA CORP.
5.8%; Score (
22.0%; Pred. 1
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23.6%;
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19.6%;
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22.0%;
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protein (VMP)2.
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d protein
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.4e+02;
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.3e+02;
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, BRIGHAM & )

sest Local Similarity

RESULT 1350

ID ABB98140 stand

DE Human PMM**

PN WO2^^
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ID ABU41908 stand DE Protein FD WO2001
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ID AAY7024
DE Human P
PN WO20001
PD 09-MAR-
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RESULT 1348
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(BECK/) BECKER J M.
(HAUS/) HAUSER M.
(DONH/) DONHARDT A.
(BARN/) BARNES D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABU41908 standard; protein; 695 AA. Protein encoded by Prokaryotic esse WO200277183-A2.
                        (CAOY/) CAO Y.
(HINK/) HINKLE G :
(SLAT/) SLATER S :
(CHEN/) CHEN X.
                                                          Bacterial polypeptide #22547.
US2003233675-Al.
18-DEC-2003
                                                                                                                                                               Saccharomyces cerevisiae OPT WO200052162-A2.
                                                                                                                                                                                                                                                                                                          AAY70245 standard;
Human Polycystin-L
WO200012046-A2.
                                                                                                                                                                                                                                                                                                                                                                            ABU43821 standard; protein; 801 Protein encoded by Prokaryotic WO200277183-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Maize oil-associated gene protei US2004075707
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 03-OCT-2002.
(ELIT-) ELITRA PHARM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO2004039405-A1
                                                                                                                                                                                                      (INCY-) INCYTE GENOMICS INC.
ry Match 5.8%;
t Local Similarity 19.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 JS2004025202-A1.
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CY Match 5.8%; Score
Local Similarity 20.4%; Pred
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(RAVA/) RAVANELLO M.
(SAVA/) SAVAGE T.
                                                                                                                                                                                                                                                                                                                                                           ELIT-) ELITRA PHARM
                                                                                                                                                                                                                                                                                                                                                                                                                              ROGE/) ROGERS J A.
                                                                                           Local Similarity
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                                                                                                             Match
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Similarity
                GOLDMAN B S
                                O G
                                                                                                                                                                                                                                                protein; 863 AA.
ID 7484157CD1.
                                                                                                                                                                                                                                                                                                                  protein; protein.
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5.8%;
24.5%;
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5.8%;
19.9%;
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5.8%;
24.3%;
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21.0%;
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22.7%;
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T protein
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Pred. No. 1.
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ن. 1.9e+02;
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.1e+02;
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.8e+02;
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.5e+02;
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DB 8;
.1e+02;
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.9e+02;
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        877;
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Best Local Similarity
RESULT 1354
ID ABU16635 standard; p
DE Protein encoded by P
PN W0200277183-A2.
PD 03-OCT-2002.
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ID AAG7076
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RESULT 1358
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RESULT 1360
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WO9702346-A2.
23-JAN-1997.
                                                                                                                       Human heat mitochondrial protein w02003087768-A2.
                                       ADL61289 standard;
Human ATP-binding of
WO2004020583-A2.
                                                                                                                                                                                                                                                                                                                                                                             AAW46761 standard; protein; 1684 AA.
Amino acid sequence of human ATP binding
WO9748797-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAG70761 standard;
S cerevisiae apopt
WO200102550-A2.
                                                                                                                                                                                                                Homo sapiens i
EP1217066-A1.
                                                                                                                                                                                                                                                                                                        AAW46771 standard; protein; 1704
Amino acid sequence of human ATP
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ry Match 5.8%; 
t Local Similarity 24.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADA34462 standard; protein; 1028 AA. Acinetobacter baumannii protein #1623. US6562958-B1.
13-MAY-2003.
                                                                                                                                                                                                       26-JUN-2002.
                                                                                                                                                                                                                                    ABP52094 standard;
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                                                                                                    (BUCK-)
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(BRIM ) BRISTOL-MYERS SQUIBB 5.8%; Local Similarity 20.3%;
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(BUCK-) BUCK INST
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ABC transporter ABCA3 p
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city 24.4%;
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                                                 protein;
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Prokaryotic essential
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sis associated p
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.3e+02;
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.3e+02;
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.7e+02;
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                                                                                                                                                                  Human ovary-specific O1-236 WO200288314-A2.
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AAB21047 standard; protein;
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WO2003048304-A2.
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                 EP1347046-A1.
                       ADM03849 standard; protein; 214 AA. Human protein of the invention SEQ
                                                                                            Human nucleoplasmin WO2003091400-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                ABM62108 standard;
                                                                                                              ADJ63172 standard;
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(AMHP ) WYETH.
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3. pneumoniae LPLC
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WO2003033515-A1.
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ASSOC BIOTECHNOLOGY.
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protein.
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n (Npm2) protein.
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antigenic protein SEQ
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26.6%;
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immunogenic
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protein,
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                                                                   AAW97221 standard; peptide; 370 AA.
Human pituitary-derived G protein-coupled
W09858962-A1.
                                                                                                                                                   AAW95181 standard; peptide; 370 AA. Human G-protein coupled rceptor polypeptide W09899295-A1.
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(INSP) INST PASTEUR.
(CNRS ) CNRS CENT NAT RECH SCI.
(CNRS ) SCORE
19 8%; Pred.
          AAG04119 standard;
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Human pituitary G-protein co
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Arabidopsis thaliana
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ABO61901 standard; protein; 472 AA. Klebsiella pneumoniae polypeptide s US6610836-B1. 26-AUG-2003.
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Human GPCR GPR10, S
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13-MAY-2004.
(PRIM-) PRIMAL INC.
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(LIFE-) LIFESPAN BIOSCIENCES
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                                                      Human dJ37C10.3 ATPase WO200157188-A2. 09-AUG-2001. (HYSE-) HYSEQ INC.
                                                                                                                              Arabidopsis thaliana EP1033405-A2. 06-SEP-2000.
                                                                                                                                                                                                       AAE05101 standard; protein; 641 AA.
Drosophila melanogaster dmKSNF.
WO200149848-A2.
12-JUL-2001.
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Human protein WO200157190-A2
       AAM79751 standard;
Human protein SEQ
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                                                                                                                                                                     OSPF-related Hepatitis C virus (HCV) 08-73N-707-108-13N-707-108-13N-707-1
                                                                                                                                                                                                                                                                                                                                                    Human diagnostic and therapeutic pprotein WO2004023973-A2.
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(HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAB42779 standard;
Human ORFX ORF2543
WO200058473-A2.
                                                                                               ADM68764 standard; protein; 5127 AA.
Peregrinus maidis ryanodine receptor protein
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(CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABO52988 standard; protein; 791 AA.
Human putative spliceosome associated protein (SAP)
US2003068803-A1.
         ADH85829 standard; protein; 178 AA.
Enterococcus faecalis polypeptide #
                                                                                                                                                                                                                                                                   Herbicidally active WO200210210-A2.
                                                                                                                                                                                                                                                                                        ABB90877 standard; protein;
                                                                                                                                                                                                                                              (FARB ) BAYER AG.
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Y Match 5.8%; Score 69;
Local Similarity 20.1%; Pred. No.
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RESULT 1409
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RESULT 1416
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(DOUC/) DOUCETTE-STAMM L
(BUSH/) BUSH D.
                                                                                                                                                                                                                                                                                                                                   ADF07413 standard; protein;
Bacterial polypeptide #3526
US6605709-B1.
12-AUG-2003.
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Arabidopsis thaliana
EP1033405-A2.
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                           ABB99751 standard; protein; 327 AA. Amino acid sequence of bacteriophage W0200295413-A2:
                                                                                                        Protein encoded WO200277183-A2.
                                                                                                                 ABU29281 standard;
Protein encoded by
                                                                                                                                                                                   ADA14398 standard; protein; 278 AA. Mouse spermatogenesis related protein W02003068969-A1.
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Actinobacillus actinomycetemcomitans
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h 5.7%; Score 6
Similarity 29.2%; Pred. N
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DE Brassica PN WO20*

PD WO20*
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RESULT 1420
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LT 1418
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30-MAR-2000.
                                      Rat-edg, G-protein
US5856443-A.
                                                                                                                                                                                                                                                                                                                          Mouse protein sequence mCP20760. WO2003073826-A2.
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Xenopus melatonin 1
WO9704094-A1.
                                                                                                             p(rat-edg),
US5585476-A.
                                                                                                                                                                                    Mouse cancer ass WO2004074321-A2.
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                                                        AAW87791 standard;
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(MACL/) MACLENNAN A
                                                                                                                               AAW01664 standard;
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                                                                                                                                                                                                                                         (PRIM-) PRIMAL INC
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                     MACLENNAN A
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SEQ ID NO:387.
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88;
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88;
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             383;
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RESULT 1426
ID ABU6181
DE Rat-edg
PN US65184
PD 11-FEB-
PA (MACL/)
                                                                                                                                         Best Local Similarity RESULT 1434
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RESULT 1428
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NESULT 1430
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28-DEC-1995.
(MASS-) MASSACHUSETTS GEN HOSPITAL.
EXTENSION OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAB66619 standard; protein; 411 AA.
Human PAC 1 receptor isoform 30.
WO2001.07478-A1.
01-FEB-2001.
                                                                                              ADS12084 standard;
Human therapeutic
                                                                                                                                                                                                                                                             ADA33815 standard; protein; 437 Acinetobacter baumannii protein
                                                                                                                                                                                                                                                                                                                                                                                                               Angiotensin converting WO200136632-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAU02941 standard;
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WO9850531-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADH87117 standard; protein; 417 Enterococcus faecalis polypeptic US6617156-B1.
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                                                                                                                                                                                                                                              US6562958-B1.
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                                                                               WO2004080148-A2.
                                                                                                                                                                                                                           13-MAY-2003
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                                      (NUVE-) NUVELO INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ocal Similarity
                                                                                                                                                          GENOME THERAPEUTICS CORP.
h 5.7%; Score
Similarity 20.5%; Pred.
Similarity
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                                                                                              ; protein; contig pro
                                                                                                                                                                                                                                                                                                                                                                                                                                protein; 431 AA.
:ing enzyme (ACEV)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           protein;
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23.6%;
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23.2%;
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29.9%;
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29.9%;
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19.8%;
5.7%;
19.6%;
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No. 1.
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No.
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1e+۱
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.1e+02;
DB 8;
.1e+02;
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+02;
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Standard

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Best Local Similarity
RESULT 1441
ID ADJ65810 standard; p
DE Human corticotropin-
PN US2004039173-A1.
PD 26-FEB-2004.
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ID AAB71866 s
DE Human CRPI
PN WC20010932
PD 08-FEB-200
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ID ABR4305
DE Human C
PN WO20030
PD 27-MAR-
PA (UYTE-)
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ID
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RESULT
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ID AB
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            02-JAN-2003.

(NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.

(ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATI
5.7%; Score 68.5; DB 7;
sry Match
5.7%; Pred. No. 1.1e+02;
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                                                                                                                                                                                           ADJ65810 standard; protein; 444 AA.
Human corticotropin-releasing facto
                                                                                                                                                                                                                                                                                                                                                                                                                   ABG76402 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human corticotropin-releasing US6495343-B1.
AAR58668 standard; protein; 448
                                                                                ADC86255 standard; protein; 447 AA.
Human GPCR protein SEQ ID NO:708.
EP1270724-A2.
                                                                                                                                                                                                                                                                                              WO2003016475-A2.
                                                                                                                                                                                                                                                                                                        ADE62734 standard; protein; 4
Human Protein P34998, SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                      Human hCRF-RA1, splice
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WO2003024990-A2.
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Human CRH-R1 beta protein SEQ ID NO:2.
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                                                                                                                               (SALK ) SALK INST BIOLOGICAL STUDIES.

TY Match 5.7%; Score 68.5;
Local Similarity 23.7%; Pred. No. 1
                                                                                                                                                                                                                                                                                                                                                                                            JS6482608-B1.
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FARB ) BAYER AG.
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Y Match 5.7%; Score 68.5;
Local Similarity 23.7%; Pred. No. 1.
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1438
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Y Match 5.7%;
Local Similarity 23.7%;
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5.7%; Score 68.
y 23.7%; Pred. No.
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23.7%;
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23.7%;
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G Score

G Pred.
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D NO
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ng factor receptor 2
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Pred.
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No. 1.
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No. 1.1e+02;
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. 1.1e+02;
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1.1e+02;
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1.1e+02;
                                               INCUBATIO.
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.1e+02;
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.le+02;
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.le+02;
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ADC86185 Btain...
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Human GPCR protein SEQ 1...

1 EP1270724-A2.

2 CPJAN-2003.
D 02-JAN-2003.
D 02-JAN-2003.
A (NADD.) NAT INST ADVANCED IND SCI & TECHNOLOGY.
PA (ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATION SCI & TECHNOLOGY INCUBATION SCI & TECHNOLOGY INCUBATION SCI & TECHNOLOGY INCUBATION SCI & TECHNOLOGY INCUBATION SCI & TECHNOLOGY INCUBATION SCI & TECHNOLOGY INCUBATION SCI & TECHNOLOGY INCUBATION SCI & TECHNOLOGY INCUBATION SCI & TECHNOLOGY INCUBATION SCI & TECHNOLOGY INCUBATION SCI & TECHNOLOGY INCUBATION SCI & TECHNOLOGY INCUBATION SCI & TECHNOLOGY INCUBATION SCI & TECHNOLOGY INCUBATION SCI & TECHNOLOGY INCUBATION SCI & TECHNOLOGY INCUBATION SCI & TECHNOLOGY INCUBATION SCI & TECHNOLOGY INCUBATION SCI & TECHNOLOGY INCUBATION SCI & TECHNOLOGY INCUBATION SCI & TECHNOLOGY INCUBATION SCI & TECHNOLOGY INCUBATION SCI & TECHNOLOGY INCUBATION SCI & TECHNOLOGY INCUBATION SCI & TECHNOLOGY INCUBATION SCI & TECHNOLOGY INCUBATION SCI & TECHNOLOGY INCUBATION SCI & TECHNOLOGY INCUBATION SCI & TECHNOLOGY INCUBATION SCI & TECHNOLOGY INCUBATION SCI & TECHNOLOGY INCUBATION SCI & TECHNOLOGY INCUBATION SCI & TECHNOLOGY INCUBATION SCI & TECHNOLOGY INCUBATION SCI & TECHNOLOGY INCUBATION SCI & TECHNOLOGY INCUBATION SCI & TECHNOLOGY INCUBATION SCI & TECHNOLOGY INCUBATION SCI & TECHNOLOGY INCUBATION SCI & TECHNOLOGY INCUBATION SCI & TECHNOLOGY INCUBATION SCI & TECHNOLOGY INCUBATION SCI & TECHNOLOGY INCUBATION SCI & TECHNOLOGY INCUBATION SCI & TECHNOLOGY INCUBATION SCI & TECHNOLOGY INCUBATION SCI & TECHNOLOGY INCUBATION SCI & TECHNOLOGY INCUBATION SCI & TECHNOLOGY INCUBATION SCI & TECHNOLOGY INCUBATION SCI & TECHNOLOGY INCUBATION SCI & TECHNOLOGY INCUBATION SCI & TECHNOLOGY INCUBATION SCI & TECHNOLOGY INCUBATION SCI & TECHNOLOGY INCUBATION SCI & TECHNOLOGY INCUBATION SCI & TECHNOLOGY INCUBATION SCI & TECHNOLOGY INCUBATION SCI & TECHNOLOGY INCUBATION SCI & TECHNOLOGY INCUBATION SCI & TECHNOLOGY INCUBATION SCI & TECHNOLOGY INCUBATION SCI & TECHNOLOGY INCUBATION SCI & TECHNOLOGY INCUBATION SCI & T
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(HINK/) HINKLE G :
(SLAT/) SLATER S (
(CHEN/) CHEN X.
                                                                                                       Bacterial polypeptide #6813.
US2003233675-A1.
                                                                                                                                                                                                                                                                                                                                                                (TAKE) TAKEDA CHEM IND LTD.

127 Match 5.7%;
15 Local Similarity 29.9%;
                                                                                                                                                                                                                                                                                                        AAR58669 standard; protein; 4
Human PACAP receptor type 1B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAR58671 standard; protein; 476 AA.
Human PACAP receptor type 1C mature
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ry Match 5.7%;
t Local Similarity 29.9%;
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Human PACAP receptor type 1-B2 matu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (MILL-) MILLENNIUM PHARM INC.
ry Match 5.7%;
t Local Similarity 29.9%;
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08-FEB-2001.
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GOLDMAN B
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.2e+02;
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.2e+02;
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LOCAL Similarity

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RESULT 1454
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OS-OCT-1994.
(TAKE) TAKEDA CHEM IND LTD.
(TAKE) TAKEDA CHEM IND LTD.
5.7%;
ery Match
5.7%;
29.9%;
                                                                                                                           Human novel secreted protein; 548 AA. US6420526-B1.
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(LIFE-) LIFESPAN BIOSCIENCES INC.

5.7%; Score 68.5

29.9%; Pred. No.
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31-JUL-2002.
(NEST ) SOC PROD NESTLE SA.
(NEST ) 5-7%;
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28.6%;
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Bifidobacterium longum
EP1227152-A1
ABO34523 standard; protein; 548 AA. Region of human secreted protein en US2003049618-A1.
                                                                                                                                                                                                                                                               ABP73995 standard; protein; 541 candida albicans essential prote WO200253728-A2.
11-JUL-2002.
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Human PACAP receptor type 1
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                                                                                                      (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                           (BLIT-) ELITRA PHARM INC.
ry Match 5.7%;
Local Similarity 21.7%;
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                                                                                                                                                                                                                                                                                                                                                                                    EOSB-) EOS BIOTECHNOLOGY INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQ
                                                                                                                                                                                                                                                                                                                                                       8.5; DB 7;
5. 1.4e+02;
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5. 1.2e+02;
                                                                  . 5,
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b. 1.4e+02;
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1.
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                  γģ
                                                                   DB 5;
.5e+02;
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.3e+02;
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Best Local Similarity
RESULT 1463
ID ADH74186 standard; I
DE Human secreted prote
PN US2003225248-A1.
PD 04-DEC-2003.
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Best Local S
RESULT 1461
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Best Local Similarity
RESULT 1462
                                                                                                                                                                                                                                                                   Query Match
     Human secreted protein #150. US2003225248-Al. 04-DEC-2007
                                                                                                                                                                          ADH17089 standard;
Human translation
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(RUBE/) RUBE
(ROSE/) ROSE
(SOPP/) SOPP
                                                                                                                           (SUCE-)
                                                                                                                                                          WO2003097854-A2.
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Novel human secret
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1461
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) ROSEN C A.
) SOPPET D R.
) CARTER K C.
) BEDNARIK D P.
ENDRESS G A.
                                                                                                                                                                                                                                                                 ZENG Z.
KYAW H.
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OLSEN H S.
PISCHER C L.
EBNER R.
BREWER L A.
MOORE P A.
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ZENG Z.
KYAW H.
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FISCHER C L.
EBNER R.
BREWER L A.
MOORE P A.
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YOUNG P E.
GREENE J M.
FERRIE A M.
DUAN D R.
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ROSEN C A.
SOPPET D R.
CARTER K C.
BEDNARIK D P.
ENDRESS G A.
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GREENE J M.
FERRIE A M.
DUAN D R.
                                                                                                                       SUGEN INC
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LI Y.
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secreted proteir
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initiation
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34.0%;
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34.0%;
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34.0%;
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n seq
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No. 1.
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                                                                                      3.5;
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.5e+02;
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BRE

FARKED IN THE WAKE OF

(GENO-)

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RESULT 1472
ID ABO8113
DE Pseudom
PN US65517
PD 22-APR-
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Best Local Similarity
RESULT 1464
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Best Local (
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05-OCT-1994.
(TAKE) TAKEDA CHEM IND LTD.
178;
21Y Match 5.78;
29.98;
                                                                                                                                                                                                                                                                                                                                                                                                                                    AAR58660 standard; protein;
Human PACAP receptor type 11
EP618291-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAR58662 standard; protein; 553 AA. Human PACAP receptor type 1C protein.
                                                                                                   ABU38306 standard;
Protein encoded by
                                                                                                                                                                                     ADS10834 standard; protein;
                                                                                                                                                                                                                                                                  ADP98892 standard; protein; C. albicans specific gene, cw02004056965-A2.
                                                                                                                                                                                                                                                                                                                                                              ABB11705 standard; peptide; 588 AA.
Human GABA transporter homologue, SEQ
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Human PACAP receptor type 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (HUMA-) HUMAN GENOME
                                                                                                                                                                         Human therapeutic WO2004080148-A2.
                                                                                                                                                                                                                                                                                                                                                                                            (TAKE) TAKEDA CHEM IND LTD.
ry Match 5.7%;
t Local Similarity 29.9%;
                                ABO81139 standard;
                                                                                                                                                                                                                  (ELIT-) ELITRA PHARM INC.
(ELIT-) ELITRA CANADA LTD.
5.7%;
ry Match
Local Similarity 26.2%;
                                                                                                                                                                                                                                                                                                                                           )9-AUG-2001.
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ry Match 5.7%;
t Local Similarity 29.9%;
                                                                                                                                                      NUVE-) NUVELO INC
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                                                 Local Similarity
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                                                ELITRA PHARM INC.
5.7%;
h
Similarity 26.3%;
                   aeruginosa
                             protein; 660 AA
                                                                                                    protein; 634
Prokaryotic (
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34.0%;
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34.0%;
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19.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                type 1B
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type 1-82 p
                   polypeptide
                                                                                                                                                                                                                                                                              ; 597 AA.
orf6.4254,
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B protein.
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Pred. No.
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Pred. No. 1.
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Pred.
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essential
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.5e+02;
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.5e+02;
                                                  DB 6;
.8e+02;
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.6e+02;
                                                                                                                                                                                                                                                                                                                                                                                              DB 2;
.5e+02;
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.5e+02;
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                                                                                                    gene #23833
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Best Local Similarity RESULT 1473
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Best Local Similarity
RESULT 1474
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RESULT 1475
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                                              Query Match
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                                                                                                                                            (CAOY/) CAO Y.
(HINK/) HINKLE G J
(SLAT/) SLATER S C
(CHEN/) CHEN X.
                                                                                                                                                                                                                                                                        Arabidopsis cell
WO200185946-A2.
                                                                                                                                                                                                                                                                                                                                           AAG20244 standard; protein; Arabidopsis thaliana protein EP1033405-A2.
                                                                                                                                                                                                                                                                                                                                                                                                     06-SEP-2000.
                                                                                                                                                                                                                                                                                                                                                                                                              AAG20245 standard; protein; Arabidopsis thaliana proteis EP1033405-A2.
AAB46310 standard;
H. pylori HPS115 px
WO200073502-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABB53933 standard;
                                    (GENO-) GENOME THERAPEUTICS 5.7%; t Local Similarity 20.3%;
                                                                                                                                                                                                      ADS23914 standard; protein;
Bacterial polypeptide #1294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FR2807446-A1.
                                                                            US6583275-B1.
                                                                                               ADC95469 standard;
                                                                                                                                                                                                                                                                                 AAU72535 standard; protein; 724
Arabidopsis cell cycle protein (
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(INSP ) INST PASTEU
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                                  ocal Similarity
                                                                                     faecium protein
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h
5.7%; Score 68.5;
Similarity 22.1%; Pred. No. 1.
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pylori selected
         d; protein; protein.
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22.3%;
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19.2%;
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25.9%;
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22.3%;
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22.3%;
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kup1.
                                     Score 68.5;
Pred. No. 2.
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n fragment
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d interacting
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SEQ
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                   788 AA
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No. 1.
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No. 2.
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No. 2.
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No. 2
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                                       DB 7;
.2e+02;
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                                                                                                                                                                                                                                                                                                                DB 3;
.1e+02;
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.1e+02;
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.9e+02;
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.9e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 7;
.9e+02;
                                                                                                                   DB 8;
.2e+02;
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PERMUTI

JC/) MUECKLER M.

JY Match Similarity

SULT 1485

ID AAY92110 standar*

DE Human WFS1 po'

PN W020001878*

PA (UNIV

PA (UNIV

PA (CUNIV)
 RESULT
ID AA
                                                                                                               Best Local Similarity
RESULT 1487
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RESULT 1484
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Best I
                    Best
                                                                                                                                           (UNIW ) UNIV WASHINGTON.
(PERM/) PERMUTT M A.
(INOU/) INOUE H.
(MUEC/) MUECKLER M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               07-DEC-2000.
(PLAC ) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN
(CREA-) CREATOGEN GMBH.
AAY92104 standard;
                                                                                   AAY92100 standard; protein; WFS1 polypeptide. W0200018787-A1.
                                                                                                                                                                                           AAY92109 standard; protein; 890
Human WFS1 polymorphism R456H.
WO200018787-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAY92103 standard;
Human WFS1 mutant I
WO200018787-A1.
                                                                                                                                                                                                                                                                                                 Human WFS1 polymorphism I333V.
WO200018787-A1.
                                                                                                                                                                                                                                                                                                                     AAY92110 standard; protein; 890 AA
                                                                                                                                                                                                                                                                                                                                                                                                         WO200018787-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                  AAY92107 standard; protein;
Human WFS1 mutant P504L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200018787-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAY92105 standard; protein;
Human WFS1 mutant G695V.
                                      (MUEC/) MUECKLER M.
                                               (UNIW) UNIV WASHINGTON (PERM/) PERMUTT M A. (INOU/) INOUE H.
                                                                                                                                                                                                                                                   (UNIW ) UNIV WASHINGTON.
(PERM/) PERMUTT M A.
(INOU/) INOUE H.
(MUEC/) MUECKLER M.
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(PERM/) PERMUTT M A.
(INOU/) INOUE H.
(MUEC/) MUECKLER M.
                                                                                                                                                                                                                                                                                                                                                                  UNIW ) UNIV WASHINGTON PERM/) PERMUTT M A. INOU/) INOUE H.
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(PERM/) PERMUTT M A.
(INOU/) INOUE H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MUEC/) MUECKLER M.
                  Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               protein; 885
DEL508 YVYLL.
protein;
                  5.7%;
23.8%;
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23.8%;
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23.8%;
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23.8%;
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No. 2.9e+02;
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No. 2.8e+02;
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                    .5; DB 3;
. 2.9e+02;
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2.4e+02;
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.9e+02;
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.9e+02;
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.9e+02;
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Query Match
Best Local S
RESULT 1489
                                                                                 Best Local Similarity
RESULT 1495
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Best Local Similarity
RESULT 1492
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                                                                                                          Query Match
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OZ-MAY-2002.
(CHIR-) CHIRON SPA.
(GENO-) INST GENOMIC RES.
S.7%; (
                                                                                                                                                                                                                                                                                                                                                       (CAOY/) CAO Y.
(HINK/) HINKLE G J.
(SLAT/) SLATER S C.
(CHEN/) CHEN X.
                                       AAB30730 standard; protein; 3015 AA. Amino acid sequence of chimeric Hepatitis WO200075338-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABP29861 standard; protein; 894 AA. Streptococcus polypeptide SEQ ID NO W0200234771-A2.
(USSH ) US DEPT HEALTH & HUMAN SERVICES.
ry Match 5.7%; Score 68.5;
                                                                                            (USSH) US DEPT HEALTH & HUMAN RESOURCES.

1. Particles: Stry Match 5.7%; Score 68.5; DB 2;

1. Local Similarity 25.8%; Pred. No. 4.8e+02;
                                                                                                                                                                 AAW88448 standard; protein; Caenorhabditis elegans NPC1
                                                                                                                                                                                                                                     (BLIT-)
                                                                                                                                                                                                                                                             C. neoformans amino WO2003052076-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                            ADN19015 standard; protein; 1004 AA.
Bacterial polypeptide #1668.
US2003233675-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAY92102 standard; protein; 937 AA.
Human WFS1 mutant del882fs/ter937.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABP28153 standard; protein; Streptococcus polypeptide SI WO200234771-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human WFS1 mutant P724L. WO200018787-A1.
                                                                                                                                                  WO9901555-A1.
                                                                                                                                                                                                                                                26-JUN-2003
                                                                                                                                                                                                                                                                                          ADB70303 standard;
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                                                                                                                                       14-JAN-1999
                                                                                                                                                                                                                                                                                                                                               (GOLD/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (UNIW ) UNIV WASHINGTON.
(PERM/) PERMUTT M A.
(INOU/) INOUE H.
(MUEC/) MUECKLER M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (CHIR-) CHIRON SPA. (GENO-) INST GENOMIC
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                                                                                                                                                                                                                                    ELITRA PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    UNIV WASHINGTON
                                                                                                                                                                                                                                                                          protein; 1178 AA.
o acid sequence SEQ ID NO:3347
                                                                                                                                                                                                         5.7%;
19.8%;
                                                                                                                                                                                                                                                                                                                  5.7%;
19.6%;
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5.7%;
22.9%;
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23.8%;
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23.8%;
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SEQ ID NO
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protein orthologue
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Pred.
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Pred.
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Pred.
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No. 4.
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No. 3
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No. 2
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No. 2.9e+02;
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.1e+02;
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.2e+02;
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.4e+02;
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.9e+02;
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  4.
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                                                      clone pH77CV-J6S.
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  3015;
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regist Staber

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protein; 247 AA.

protein fragment SEQ ID NO

20-UUN-2001.

PA (KYOW) KYOWA HAKKO KOGYO KK.

Query Match
Best Local Similarity 23.1%; Pred. No. 55;

RESULT 1500

ID AAY41212 standard; protein; 250

E Coli MttB polypeptid

PN W09951753-A1.

PD 14-OCT-10
                                                                                                                                                                                                                                                                                                                                                                Query Match

Best Local Similarity 23.5%; F

RESULT 1498

ID AAB78946 standard; protein; 24

DE C. glutamicum SRT protein sequ

PN WC200100804-A2.

PD 04-JAN-2001.

PA (BADI) BASF AG.
                                                                                                                                                                                                  Query Match
Best Local Similarity
RESULT 1499
ID AAG91355 standard; pr
DE C glutamicum protein
PN EP1108790-A2.
PD 20-UUN-2001.
PA (KYOW) KYOWA HAKKO K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 26.7%; Pred. No. 1.5e+03; RESULT 1496

ID AAB30732 standard; protein; 3015 AA.

DE Amino acid sequence of chimeric Hepatitis C viru W0200075338-A2.

PD 14-DEC-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAB30732 standard; protein; 3015 AA.
Amino acid sequence of chimeric Hepatitis C virus clone J6S.
W0200075338-A2.
14-DEC-2000.
(USSH ) US DEPT HEALTH & HUMAN SERVICES.
STY Match
STY Match
STY Score 68.5; DB 4; Length 3015;
BT LOCAL Similarity 26.7%; Pred. No. 1.5e+03;
                                                                                                                                                                                                                                      AAG91355 standard; protein; 247 AA.
C glutamicum protein fragment SEQ ID NO: 5109.
EP1106790-A2.
                                                                                                                                                                                                                                                                                                                                                              AAB78946 standard; protein; 247 AA.
C. glutamicum SRT protein sequence SEQ ID NO:152.
WO200100804-A2.
04-JAN-2001.
(BADI ) BASF AG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADK16845 standard; protein; 200 AA.
Nanoarchaeum equitans cancer-associated (CA) protein #398.
W02003093434-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (DIVE-) DIVERSA CORP.
  Local Similarity
5.7%;
23.0%;
                                                                                                                                                                                                                                                                                                                      5.7%; Score 68; DB 4; Length 247; 23.1%; Pred. No. 55;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 68; DB 8; Pred. No. 41;
  Score 68;
Pred. No.
  DB 2;
                                                                                                                                                             DB 4;
55;
                    Length 258;
                                                                                                                                                                                Length 247;
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Perfect score:
Sequence:
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 GenCore version 5.1.6 (c) 1993 - 2005 Compugen Ltd.
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US-10-223-083-62

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US-10-156-239-17
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US-10-156-239-17
US-10-199-485-17
US-10-199-485-17
US-10-199-38-703-9
US-09-938-703-9
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US-09-938-703-9
US-10-612-791-9
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